

83844

STIC-Biotech/ChemLib

From: Bugaisky, Gabriele
Sent: Wednesday, January 08, 2003 1:29 PM
To: STIC-Biotech/ChemLib
Subject: 09/943692

please search SEQ ID NO:2 and truncations thereof >530 aa.

thanks, gabi

Gabriele E. Bugaisky
* au 1653
* cml-10d09; mailbox 9b01
* 308-4201

Gabi,
truncations >530 should be
retrieved in the standard search.
However, I thought an digomer search
might also be helpful, since it provides
a list of seqs that contain ^{areas of} contiguous
100% matches to the query seq. Hits are
listed in decreasing order of the length
of the 100% match region.
Barb

Point of Contact:
Barb O'Brien
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 1-10-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: January 10, 2003, 10:44:24 ; Search time 39 Seconds
(without alignments)
2200.344 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406
Sequence: 1 MNPNRSEHDITKTENNEV.....TGLSAGKRVYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	644	8 AAP70085	Sequence of toxin
2	3406	100.0	644	9 AAP82487	Delta endotoxin en
3	3406	100.0	644	10 AAP94679	Amino acid sequenc
4	3406	100.0	644	10 AAP95585	M-7 crystal toxin.
5	3406	100.0	644	14 AAR39751	Delta endotoxin.
6	3406	100.0	644	15 AAR56697	CryIIA insecticida
7	3406	100.0	644	15 AAR56698	CryIIB insecticida
8	3406	100.0	652	20 AAR53214	Amino acid sequenc
9	3403	99.9	644	17 AAR99960	B.t.t. coleopteran
10	3403	99.9	644	18 AAW34817	Novel CryIIIA muta

11	3403	99.9	644	18 AAW34827	Novel CryIIIA muta
12	3403	99.9	644	18 AAW34829	Novel CryIIIA muta
13	3403	99.9	644	18 AAW34841	Novel CryIIIA muta
14	3402	99.9	644	18 AAW34822	Novel CryIIIA muta
15	3402	99.9	644	18 AAW34828	Novel CryIIIA muta
16	3401	99.9	644	18 AAW34812	Novel CryIIIA muta
17	3401	99.9	644	18 AAW34820	Novel CryIIIA muta
18	3401	99.9	644	18 AAW34832	Novel CryIIIA muta
19	3401	99.9	644	18 AAW34834	Novel CryIIIA muta
20	3401	99.9	644	18 AAW34835	Novel CryIIIA muta
21	3401	99.9	644	18 AAW34836	Novel CryIIIA muta
22	3400	99.8	644	18 AAW34813	Novel CryIIIA muta
23	3400	99.8	644	18 AAW34818	Novel CryIIIA muta
24	3400	99.8	644	18 AAW34821	Novel CryIIIA muta
25	3400	99.8	644	18 AAW34825	Novel CryIIIA muta
26	3400	99.8	644	18 AAW34826	Novel CryIIIA muta
27	3400	99.8	644	18 AAW34830	Novel CryIIIA muta
28	3400	99.8	644	18 AAW34840	Novel CryIIIA muta
29	3398	99.8	644	17 AAR99958	Bacillus thuringie
30	3398	99.8	644	18 AAW34814	Novel CryIIIA muta
31	3398	99.8	644	18 AAW34815	Novel CryIIIA muta
32	3398	99.8	644	18 AAW34816	Novel CryIIIA muta
33	3398	99.8	644	18 AAW34823	Novel CryIIIA muta
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36	3398	99.8	644	18 AAW34833	Novel CryIIIA muta
37	3398	99.8	644	18 AAW34839	Novel CryIIIA muta
38	3397	99.7	644	18 AAW34811	Novel CryIIIA muta
39	3397	99.7	644	18 AAW34837	Novel CryIIIA muta
40	3397	99.7	644	18 AAW34838	Novel CryIIIA muta
41	3396	99.7	644	9 AAP80467	Bacillus thuringie
42	3392	99.6	644	18 AAW34819	Novel CryIIIA muta
43	3329	97.7	644	22 AAW84195	Amino acid sequenc
44	3328	97.7	645	18 AAW34784	An artificial modl
45	3149	92.5	597	17 AAW00334	Bacillus thuringie

ALIGNMENTS

RESULT 1
ID AAP70085 standard; Protein; 644 AA.
XX AAP70085;
AC
XX
DT 04-MAY-1991 (first entry)
XX
DE Sequence of toxin which is toxic to beetles of the order
DE Coleoptera.
XX
KW Microbial pesticide.
XX
OS Bacillus thuringiensis strain san diego.
XX
PN BP213818-A.
XX
PD 11-MAR-1987.
XX
PF 08-AUG-1986; 86EP-0306151.
XX
PR 16-JUN-1986; 86US-0874727.
PR 16-AUG-1985; 85US-0767227.
PA (MYCO-) MYCOGEN CORP.
PI Herrnstadt C, Wilcox E;
XX
XX WPI; 1987-066492/10.
DR N-PSDB; AAN70092.
XX
XX New poly:peptide toxin having pesticidal activity - formed by
PT bacillus thuringiensis toxin gene, and useful for killing

PT Coleoptera beetles
 PS Claim 3; pp15-16; 19pp; English.
 CC B. thuringiensis toxin gene toxic to Coleoptera beetles is cloned
 CC and expressed. Live micro-organisms for inhibiting the growth of, or
 CC killing, the beetles are obtained. The polypeptide toxin may be isolated
 CC for use against the beetles.
 XX Sequence 644 AA;
 SQ

Query Match 100.0%; Score 3406; DB 8; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEVPINHOYPLAETPNPTLEDLNYKEFLRTADNNTALDSS 60
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 DB 61 TTKDVIQKGISVVDLLGVGFPFGALVSYFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
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 DB 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLTVLDLALFPLDYVRLYPREKTELT 300
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 DB 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 QY 421 KVEFSQVNDQDEASTQYDSKRNVGAVSWDSIDOLPPEPTTDEPLEKGYSHQNLNYMCEL 480
 DB 421 KVEFSQVNDQDEASTQYDSKRNVGAVSWDSIDOLPPEPTTDEPLEKGYSHQNLNYMCEL 480
 QY 481 MOGSRGITPVLWTWTHKSVDFPNMIDSKITQLPLVAKAYKLGASAVYAGPRFTGGDIIOC 540
 DB 481 MOGSRGITPVLWTWTHKSVDFPNMIDSKITQLPLVAKAYKLGASAVYAGPRFTGGDIIOC 540
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 DB 541 TEMGSAATIVTVDVYSOKYRARIHASTSOITFTLSLDGAFNOYFEDKTIINKGDTLT 600
 QY 601 YNPFNLASFSTPELGSNNLOIGVTGLSAGDKYIDKIEFIPVN 644
 DB 601 YNPFNLASFSTPELGSNNLOIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 2
 AAP82487
 ID AAP82487 standard; protein; 644 AA.
 XX
 AC AAP82487;
 XX
 DT 01-NOV-1990 (first entry)
 XX
 DE Delta endotoxin encoded by cryC.
 XX
 KW Coleoptera; toxin; cryC; insecticide; delta-endotoxin; Lepidoptera.
 XX
 OS Bacillus thuringiensis EG2158.

XX
 FH Key Location/Qualifiers
 FT Reptide 1..53
 FT /label=signal_peptide
 FT /note="6 kD"
 FT Protein 54..644
 FT /label=mature_toxin
 XX
 PN MO8808880-A.
 XX
 PD 17-NOV-1988.
 XX
 PE 04-MAY-1987; 87W0-US01495.
 XX
 PR 06-MAY-1987; 87US-0047945.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Donovan WP, Gonzales JM, Levinson BL, Macaluso A;
 XX
 DR WPI: 1988-338229/47.
 XX
 DR N-PSDB; AAP82139.
 XX
 PT New gene encoding delta endotoxin of *Bacillus thuringiensis* -
 PT effective as insecticide against Coleoptera.
 PS Claim 10; Fig 8; 82pp; English.
 CC The cryC gene encodes a delta endotoxin which is an insecticide
 CC effective against Coleoptera and Lepidoptera. The sequence was
 CC isolated from cDNA library, on a plasmid designated pEG212. The
 CC plasmid can be used to construct an expression vector which can
 CC be used to transform *B. megaterium* ATCC 35965. Colorado potato
 CC beetle larvae treated with a suspension of cultured cells were
 CC dead within one week. The protein can be used as pure crystals
 CC or in the form of B.C. spores.
 CC See also AAP82141.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 9; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEVPINHOYPLAETPNPTLEDLNYKEFLRTADNNTALDSS 60
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 DB 61 TTKDVIQKGISVVDLLGVGFPFGALVSYFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
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 DB 121 IADYAKKALAELOGLONNVEDYVSSWQKNPVSSRNHSGRIRELSQASHFRNS 180
 QY 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAPFYKROLKTJOEYT 240
 DB 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAPFYKROLKTJOEYT 240
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 DB 301 RDVLTDPVGNVNLRGYGTFSNIENYIRKPHLEFDYLHRIQFHTROPQGYGNDSEFNYS 360
 QY 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
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Db 421 KVEFSQYNOQTDEASTQYDTSKRNVGAVSWDSIDQLPPTTDEPLEKGYSHQINVMCEFL 480
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Db 541 TENGSAATIVTPDVASQYKRYARIHYASTQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKYIDKIEFIPVN 644
Db 601 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 3
AAP94679
ID AAP94679 standard; protein; 644 AA.
AC AAP94679;
XX 17-JUL-1990 (first entry)
DE Amino acid sequence of the Btl3 protein.
XX Bacillus thuringiensis tenebrionis; 66 kDa crystal protein; btl3 gene;
KM Btl3 protein; toxin; Coleoptera; p1VE38.
XX Bacillus thuringiensis.
XX Key Location/Qualifiers
FH 58..79
FT Region /note="N-terminal residues of the Btl3 protein"
FT Misc-difference 58 /note="This residue was not unambiguously determined.
FT /note="It could possibly be Ser."
FT Misc-difference 60 /note="As above. It could possibly be Pro."
FT Misc-difference 64 /note="As above. It could possibly be Gln."
XX W08901515-A.
XX 23-FEB-1989.
XX 15-AUG-1988; 88WO-EP00752.
XX 29-DEC-1987; 87GB-0030261.
XX (PLAN-) PLANT GENETIC SYSTEMS.
XX Vaecck M, Hofte H, Botterman J;
XX WPI: 1989-068871/09.
XX N-PSDB; AAN91071.
XX Plant cell transformed with DNA -
XX is for Bacillus thuringiensis toxic protein and is resistant to
XX Coleoptera pests
XX Disclosure; : 35pp; English.
XX The btl3 gene encodes a 66 kDa crystal protein (the Btl3 protein) which
XX is believed to be the active protein in the crystal toxin (the Btl3
XX toxin) produced by Bacillus thuringiensis (B.t.) tenebrionis and B.t.
XX S1. The patent is for a transformed plant cell which includes, inserted
XX in its genome, the btl3 gene, or a fragment which encodes the 66kD
XX crystal protein. Plant cells contg. DNA encoding this protein are
XX protected against Coleoptera. Also new are plants (and their seeds)
XX contg. these cells; a specific DNA sequence of 1760 b; the crystal
XX protein; and microorganisms transformed with the DNA.

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SQ Sequence 644 AA:
Query Match 100.0%; Score 3406; DB 10; Length 644;
Best Local Similarity 100.0%; Pred. 1.7e-268;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 GNYVSTRPSIGSNDITTSPEYGNKSEPEONLEFNEKRYRAVANTNLAVMPSAYISGVT 420
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Db 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVAKYKQASASVYAGPRTGGDIIOC 540
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QY 601 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKYIDKIEFIPVN 644
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RESULT 4
AAP95585
ID AAP95585 standard; protein; 644 AA.
AC AAP95585;
XX 08-AUG-1990 (first entry)
XX M-7 crystal toxin.
XX M-7 toxin crystal; Coleoptera; beetle.
XX Bacillus thuringiensis strain san-diego (NRRL B-15939).
XX US4853331-A.
XX 01-AUG-1989.
XX 30-NOV-1988; 88US-0278292.
XX 16-AUG-1985; 85US-0767227.
XX 15-JUL-1988; 88US-0219420.

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XX (MYCO-) MYCOGEN CORP.
 XX Hernstadt C, Wilcox E;
 XX WPI: 1989-277854/38.
 XX N-PSDB: AAN90957.
 XX Cloning of *Bacillus thuringiensis* toxin gene
 XX for expression of protein toxic to beetles of order Coleoptera.
 XX
 PS Disclosure; Page 13-14; 10pp; English.
 CC The gene encoding the toxin can be cloned and used to produce the
 CC M-7 crystal which has activity against eg western spotted cucumber
 CC beetle, and northern, western and southern corn rootworm.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 10; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MNPNNRSEHDITKTENNEVPTNHYOYPLAETPNPTLEDLNYKEFLRMTADNTEALDSS 60
 QY 61 TTKDVIQKGISVVDLGVGFPGGALVSFTYNTFLTIPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVDLGVGFPGGALVSFTYNTFLTIPSEDPMKAFMEQVEALMDOK 120
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 DB 121 IADYAKKNAALAEIQLQNNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
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 DB 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRQKLTQEYT 240
 QY 241 DHCYKWTNGLDKLRGSSYESWVNFNRYRREMTLTVDLALPLVDVRLPREVTELT 300
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 DB 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIYVN 644

XX 28-JAN-1994 (first entry)
 XX Delta endotoxin.
 XX Endotoxin; *Bacillus*; lice; insecticide; sheep.
 XX *Bacillus thuringiensis* PS40D1.
 XX WO9314641-A.
 XX
 XX 05-AUG-1993.
 XX
 XX 31-DEC-1992; 92WO-US11337.
 XX
 XX 29-JAN-1992; 92US-0828788.
 XX
 XX (MYCO) MYCOGEN CORP.
 XX
 XX Hickie LA, Payne J;
 XX WPI: 1993-258266/32.
 XX N-PSDB: AAQ47288.
 XX
 XX Controlling biting lice on sheep - comprises administering
 XX *Bacillus thuringiensis* toxins to host
 XX
 PS Disclosure; Page 31-32; 64pp; English.
 CC Many strains of *Bacillus thuringiensis* (B.t) produce insecticidal
 CC delta endotoxins. A number of these endotoxins have been found to
 CC be toxic to *Damiliia* ovis, the biting louse of sheep. The B.T.
 CC isolates which produce these toxins can be grown and the delta
 CC endotoxin which is produced can be recovered by standard procedures.
 CC The genes encoding these endotoxins can also be transferred to a
 CC suitable host via a recombinant vector and the resulting
 CC transformants used in methods to control lice.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 14; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPTNHYOYPLAETPNPTLEDLNYKEFLRMTADNTEALDSS 60
 DB 1 MNPNNRSEHDITKTENNEVPTNHYOYPLAETPNPTLEDLNYKEFLRMTADNTEALDSS 60
 QY 61 TTKDVIQKGISVVDLGVGFPGGALVSFTYNTFLTIPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVDLGVGFPGGALVSFTYNTFLTIPSEDPMKAFMEQVEALMDOK 120
 QY 121 IADYAKKNAALAEIQLQNNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
 DB 121 IADYAKKNAALAEIQLQNNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
 QY 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRQKLTQEYT 240
 DB 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRQKLTQEYT 240
 QY 241 DHCYKWTNGLDKLRGSSYESWVNFNRYRREMTLTVDLALPLVDVRLPREVTELT 300
 DB 241 DHCYKWTNGLDKLRGSSYESWVNFNRYRREMTLTVDLALPLVDVRLPREVTELT 300
 QY 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGDSFNYS 360
 DB 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGDSFNYS 360
 QY 361 GNYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 QY 421 KYEFSQYNDQTEASTQYDSKRNGAVSMDSIDQLPETTDEPLEKGYSHQUNYMCFL 480

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Db 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPETTDEPLEKGYSHQLNVMCF 480
Oy 481 MGSRGCTIPVLWTWTHKSVDFEPMIDSKKITQPLVAKAKLOGSASVAGPRTGGDIIOC 540
Db 481 MGSRGCTIPVLWTWTHKSVDFEPMIDSKKITQPLVAKAKLOGSASVAGPRTGGDIIOC 540
Oy 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Db 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Oy 601 YNSFNLFASFSTPELSCGNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLFASFSTPELSCGNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

RESULT 6
AAR56697
ID AAR56697 standard; Protein; 644 AA.
AC AAR56697;
XX
DT 27-MAR-1995 (first entry)
XX
DE CryIIIA insecticidal crystal protein.
XX
KW CryIIA: CryIIB: CryIC: P-2: CryBI: insecticidal protein crystal;
KW lepidoptera: environmental insecticide; Bacillus thuringiensis; toxic;
KW probe: hybridisation.
XX
OS Bacillus thuringiensis.
XX
PN US5338544-A.
XX
PD 16-AUG-1994.
XX
PF 16-APR-1987; 87US-0039542.
XX
PR 16-APR-1987; 87US-0039542.
PR 11-JUL-1989; 89US-0379015.
PR 28-AUG-1991; 91US-0751452.
PR 26-FEB-1993; 93US-0023736.
XX
PA (ECOG-) ECOGEN INC.
XX
PI Donovan WP;
XX
DR WPI; 1994-263236/32.
DR N-PDB; AAQ71026.
XX
PT New Cry IIB protein - obd. from the cry II B gene in Bacillus
PT thuringiensis var. Kurstaki, active against lepidopteran insects
XX
PS Example 7; Fig 4A-4D; 39pp; English.
XX
CC This sequence shows the amino acid sequence of CryIIIA protein. The
CC promoter from the CryIIA gene sequence was fused to the protein
CC coding region of the CryIIB gene (AAQ71027). The recombinant hybrid
CC fusion gene expressed the CryIIB crystal protein more efficiently
CC than its native promoter. CryIIB encodes an insecticidal crystal
CC protein isolated from Bacillus thuringiensis var. kurstaki. It
CC produces crystal proteins during sporulation which are specifically
CC toxic to certain orders and species of insects, esp. lepidoptera.
CC CryIIB can be used in compositions used as environmentally acceptable
CC insecticides. (See also AAR56696 and AAR56698)
XX
SQ Sequence 644 AA;
Query Match 100.0%; Score 3406; DB 15; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.7e-268;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MNPNNRSEHDITIKTENNEVPTNHOYPLAETPPTLEDLNVKFEFLMTADNNTALDSS 60

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Db 1 MNPNNRSEHDITIKTENNEVPTNHOYPLAETPPTLEDLNVKFEFLMTADNNTALDSS 60
Oy 61 TTKVIOKIGISVVDLIGVGFPEGALVSEYTFELNTIMPESEDPMKAFEOVEALNDQK 120
Db 61 TTKVIOKIGISVVDLIGVGFPEGALVSEYTFELNTIMPESEDPMKAFEOVEALNDQK 120
Oy 121 IADYAKNKALAELOGLONNVEDVYSAISSWQKNPVSSRNPHSGRIRBELSQAESHRNS 180
Db 121 IADYAKNKALAELOGLONNVEDVYSAISSWQKNPVSSRNPHSGRIRBELSQAESHRNS 180
Oy 181 MSPFASISGEVLEFLTTVQAANTHLFLKDAQITGEEGKEKEDIAEFTKRLQLTQET 240
Db 181 MSPFASISGEVLEFLTTVQAANTHLFLKDAQITGEEGKEKEDIAEFTKRLQLTQET 240
Oy 241 DHCVMKNVNGDLKLGSSSESVNENRNRREMTLVLDLALFPLYDVRLYPKKVEKTEL 300
Db 241 DHCVMKNVNGDLKLGSSSESVNENRNRREMTLVLDLALFPLYDVRLYPKKVEKTEL 300
Oy 301 RDVLTDPVIGVNNLRGCTTSNIBNTYRKPHLEFDYLRHIOFHRPQGYGNDSPYWS 360
Db 301 RDVLTDPVIGVNNLRGCTTSNIBNTYRKPHLEFDYLRHIOFHRPQGYGNDSPYWS 360
Oy 361 GMYSTRPSIGSNDITTSPEYGNKSEPVONLEFNGEKYRAVANTNLAVPSAVYSGVT 420
Db 361 GMYSTRPSIGSNDITTSPEYGNKSEPVONLEFNGEKYRAVANTNLAVPSAVYSGVT 420
Oy 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPETTDEPLEKGYSHQLNVMCF 480
Db 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPETTDEPLEKGYSHQLNVMCF 480
Oy 481 MGSRGCTIPVLWTWTHKSVDFEPMIDSKKITQPLVAKAKLOGSASVAGPRTGGDIIOC 540
Db 481 MGSRGCTIPVLWTWTHKSVDFEPMIDSKKITQPLVAKAKLOGSASVAGPRTGGDIIOC 540
Oy 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Db 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Oy 601 YNSFNLFASFSTPELSCGNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLFASFSTPELSCGNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

RESULT 7
AAR56698
ID AAR56698 standard; Protein; 644 AA.
AC AAR56698;
XX
DT 27-MAR-1995 (first entry)
XX
DE CryIIB insecticidal crystal protein.
XX
KW CryIIA: CryIIIA: CryIIB: CryIC: P-2: CryBI: insecticidal protein crystal;
KW lepidoptera: environmental insecticide; Bacillus thuringiensis; toxic;
KW probe: hybridisation.
XX
OS Bacillus thuringiensis.
XX
PN US5338544-A.
XX
PD 16-AUG-1994.
XX
PF 16-APR-1987; 87US-0039542.
XX
PR 16-APR-1987; 87US-0039542.
PR 11-JUL-1989; 89US-0379015.
PR 28-AUG-1991; 91US-0751452.
PR 26-FEB-1993; 93US-0023736.
XX
PA (ECOG-) ECOGEN INC.
XX

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PI Donovan WP;
 XX WPI: 1994-263236/32.
 DR N-PSDB; AAO71027.
 XX
 PT New Cry IIB protein - obtd. from the cry II B gene in *Bacillus*
 PT thuringiensis var. *Kurstaki*, active against lepidopteran insects
 XX
 PS Claim 1: Flg 6A-6D; 39pp; English.
 XX
 CC This sequence shows the amino acid sequence of CryIIB protein. The
 CC protein from the CryIIA gene (AA071026) sequence was fused to the
 CC protein coding region of the CryIIB gene. The recombinant hybrid
 CC fusion gene expressed the CryIIB crystal protein more efficiently
 CC than its native promoter. CryIIB encodes an insecticidal crystal
 CC protein isolated from *Bacillus thuringiensis* var. *Kurstaki*. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. Lepidopterans.
 CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR56696 and AAR56698)
 CC
 SQ Sequence 644 AA:

Query Match 100.0%; Score 3406; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1,7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEPTNHHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNNEPTNHHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 QY 61 TTKDVIQKISVYVGDLLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKISVYVGDLLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSQGRIRLEFSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSQGRIRLEFSQASHFRNS 180
 QY 181 MDSFASISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEYKEKEDIAEFYKRLKTOEYT 240
 DB 181 MDSFASISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEYKEKEDIAEFYKRLKTOEYT 240
 QY 241 DHCQVWYNGGLDKLKGSSSESVNRRNRREKTLTVLDLALFPLYDVRLYKVEKTELT 300
 DB 241 DHCQVWYNGGLDKLKGSSSESVNRRNRREKTLTVLDLALFPLYDVRLYKVEKTELT 300
 QY 301 RDVLDPYIVGVNLLRGYGTTFESNIENYTRKPLFDYLRHQFPHRPOFGYGNDSFNWYS 360
 DB 301 RDVLDPYIVGVNLLRGYGTTFESNIENYTRKPLFDYLRHQFPHRPOFGYGNDSFNWYS 360
 QY 361 GNYVSTRPSIGSNDIITSPFGNKSSEPVQNLFEFNGEKYRAVANNTNLAVPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDIITSPFGNKSSEPVQNLFEFNGEKYRAVANNTNLAVPSAVYSGVT 420
 QY 421 KVEFSQVNDQDEASTQYTDKRNAGAVSMISDLPETDEPLEKGYSHQLWYVWCF 480
 DB 421 KVEFSQVNDQDEASTQYTDKRNAGAVSMISDLPETDEPLEKGYSHQLWYVWCF 480
 QY 481 MGSRGITPLVLTWTHKSVDFNMIDSKKITQLPLVKATKQSGASVAVAGPFTGDIIOC 540
 DB 481 MGSRGITPLVLTWTHKSVDFNMIDSKKITQLPLVKATKQSGASVAVAGPFTGDIIOC 540
 QY 541 TENGAATVYTPDVYSQKTRARAHVASTISQITFTSLDGAAPNQQYFEDKTIKGDILT 600
 DB 541 TENGAATVYTPDVYSQKTRARAHVASTISQITFTSLDGAAPNQQYFEDKTIKGDILT 600
 QY 601 YNSFNIAFSPTPELSGNNLQIGVTLGAGDKYVIDKIEEIPVN 644
 DB 601 YNSFNIAFSPTPELSGNNLQIGVTLGAGDKYVIDKIEEIPVN 644

RESULT 8

AAV23214
 ID AAV23214 standard; Protein; 652 AA.
 XX
 AC AAV23214;
 XX
 DT 24-AUG-1999 (first entry)
 XX
 DE Amino acid sequence of Cry3A protein.
 XX
 KW Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
 KW coleoptera; southern corn rootworm; western corn root worm; Cry3A.
 KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
 KW Diabrotica virgifera virgifera LeConte; insecticide resistance.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN W09331248-A1.
 XX
 PD 24-JUN-1999.
 XX
 PE 17-DEC-1998; 98WO-0526852.
 XX
 PR 18-DEC-1997; 97US-0996441.
 PR 18-DEC-1997; 97US-0993170.
 PR 18-DEC-1997; 97US-0993722.
 PR 18-DEC-1997; 97US-0993775.
 XX
 PA (ECOG-) ECOGEN INC.
 PA (MONS) MONSANTO CO.
 XX
 PI Brussels SM, Bryson JW, English L, Kulesza CA, Malvar TM;
 PI Romano C, Slatin SL, Von Tersch MA, Walters FS;
 XX
 DR WPI: 1999-395184/33.
 XX
 PT Insecticidal *Bacillus thuringiensis* proteins
 XX
 PS Disclosure; Page 505-507; 512pp; English.
 XX
 CC The present sequence represents the Cry3A protein. The specification
 CC describes new *Bacillus thuringiensis* Cry3B mutant proteins, and
 CC provides methods for producing them. The B. *thuringiensis* Cry3B
 CC polypeptide was modified to have improved insecticidal activity or
 CC enhanced insecticidal specificity against a target insect. The
 CC modification comprises at least one amino acid substitution, addition,
 CC or deletion in the primary sequence of the native or unmodified Cry3B
 CC polypeptide, wherein the substitution or deletion occurs at a position
 CC corresponding to from about amino acids 1-365 of the unmodified
 CC polypeptide sequence (AAV23207 represents the wild type Cry3B
 CC protein). The polypeptide can be used to kill coleopteran pests,
 CC especially by application to the environment. It is especially
 CC useful against southern corn rootworm and western corn root worm,
 CC (*Diabrotica undecimpunctata* howardi Barber, and *Diabrotica virgifera*
 CC *virgifera* LeConte respectively). The mutant cry3B polynucleotides
 CC can also be used to produce transgenic plants with increased
 CC insecticide resistance.
 CC
 SQ Sequence 652 AA:

Query Match 100.0%; Score 3406; DB 20; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1,7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEPTNHHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 9 MNPNNRSEHDITKTENNNEPTNHHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 68
 QY 61 TTKDVIQKISVYVGDLLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 DB 69 TTKDVIQKISVYVGDLLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 128
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSQGRIRLEFSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSQGRIRLEFSQASHFRNS 180


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DB 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
|||||
RESULT 10
AAW34817
ID AAW34817 standard; Protein: 644 AA.
XX
AC AAW34817;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein SA13A.
XX
KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KM relative solvent accessibility; plant resistance;
KM Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 413 /label= S413A
FT /note= "wild type Ser replaced with Ala"
XX
PN US5659123-A.
XX
PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
PI Jansens S, Peferoen M, Van Rie J;
XX
DR WPI; 1997-424316/39.
XX
PT Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page : 22pp; English.
XX
CC Novel CryIIIA proteins AAW3481-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The BC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.93 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA:

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Query Match 99.9%; Score 3403; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 2,9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 MNPNRSEHDTIKTENNEVPNTNHVOYPLAETPNPTLEDNLNKEFLRMTADNNTALDSS 60
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DB 1 MNPNRSEHDTIKTENNEVPNTNHVOYPLAETPNPTLEDNLNKEFLRMTADNNTALDSS 60
OY 61 TTKDVIQKISVVDGLGVGPFPGGALVSPFTNPLNTIMPSEDPWKAFMQVEALDQK 120
DB 61 TTKDVIQKISVVDGLGVGPFPGGALVSPFTNPLNTIMPSEDPWKAFMQVEALDQK 120
OY 121 IADYAKNKAALAELOGLQNNVEDYVSLSSWQKNPVSSNPNHSGRIRLFFSQASHFRNS 180
DB 121 IADYAKNKAALAELOGLQNNVEDYVSLSSWQKNPVSSNPNHSGRIRLFFSQASHFRNS 180
OY 181 MPEFALISGEVLEFLTTYQAANTHFLFKDAQIYGEEMGKEDIAEFKKQLTQET 240
DB 181 MPEFALISGEVLEFLTTYQAANTHFLFKDAQIYGEEMGKEDIAEFKKQLTQET 240
OY 241 DHCVMWVWNGDLKLGSSYESVWNNRFRRENTLVLDLFLPYDVRLLPKVKELT 300
DB 241 DHCVMWVWNGDLKLGSSYESVWNNRFRRENTLVLDLFLPYDVRLLPKVKELT 300
OY 301 RDVLDPPIVGVNNLNGYGTFSNIENYIRKPHLEFDLHRIGFHTRFQGYGNDSPNWS 360
DB 301 RDVLDPPIVGVNNLNGYGTFSNIENYIRKPHLEFDLHRIGFHTRFQGYGNDSPNWS 360
OY 361 GNYVSTRPSISGNDIITSPFGNKSSEPVQULEFNGEYVRAVANTNLAVPSPVSGVT 420
DB 361 GNYVSTRPSISGNDIITSPFGNKSSEPVQULEFNGEYVRAVANTNLAVPSPVSGVT 420
OY 421 KYEFQYNDQDDEASTQYDYSKRNGAVSWDSIDOLPETTDEPLEKGSYHQLVYVWCF 480
DB 421 KYEFQYNDQDDEASTQYDYSKRNGAVSWDSIDOLPETTDEPLEKGSYHQLVYVWCF 480
OY 481 MGSRGITPVLTWTHKSVDFNMIDSKKITQLPLKAVKLGASVYVAGPRTGGDIIOC 540
DB 481 MGSRGITPVLTWTHKSVDFNMIDSKKITQLPLKAVKLGASVYVAGPRTGGDIIOC 540
OY 541 TENGSAAITTYTPDVSYSOKYRARIHVASTQITFTSLDAPRNQYFEDKTIKGTLT 600
DB 541 TENGSAAITTYTPDVSYSOKYRARIHVASTQITFTSLDAPRNQYFEDKTIKGTLT 600
OY 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

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RESULT 11
AAW34827
ID AAW34827 standard; Protein: 644 AA.
XX
AC AAW34827;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein S385A.
XX
KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 385 /label= S385A
FT /note= "wild type Ser replaced with Ala"
XX
PN US5659123-A.
XX
PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.

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PA	(PLBZ) PLANT GENETIC SYSTEMS NV.
XX	
XX	Jansens S, Peferoen M, Van Rle J;
PI	
DR	WPI: 1997-424316/39.
XX	
PT	Modified Bacillus thuringiensis CryII proteins - With increased
PR	toxicity against insect pests, particularly Coleopteran insects,
XX	e.g. corn rootworm and Colorado potato beetle
PS	
XX	Example 1; Page -: 22pp; English.
CC	
CC	Novel CryIIIA proteins AAW4811-41 were produced by alanine scanning
CC	mutagenesis of domain II of the CryIIIA protein of Bacillus
CC	thuringiensis. All the positions changed to alanine in these proteins
CC	are located in some of the solvent exposed loops and beta-strands
CC	directed towards or located at the molecular apex. The substituted amino
CC	acids have a relative solvent accessibility of at least 40%, or are a
CC	maximum distance of 3 amino acids away from an amino acid having at least
CC	40% relative solvent accessibility. The novel CryIIIA proteins have an
CC	increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC	and can be used to combat, or improve plant resistance towards insects.
CC	Specifically, the toxicity of the present sequence towards Diabrotica
CC	virgifera virgifera was tested. The EC50 value (concentration at which
CC	50% feeding inhibition is observed) of the present protein was found to
CC	be 0.78 microgram per millilitre, compared to 2.88 microgram per
CC	millilitre for the wild type CryIIIA protein.
CC	Note: this sequence does not appear in the specification; it was created
CC	using information provided.
XX	
SQ	
SQ	Sequence 644 AA:
Query Match	99.9%; Score 3403; DB 18; Length 644;
Best Local Similarity	99.8%; Pred. No. 2.9e-268;
Matches 643; Conservative	1; Mismatches 0; Indels 0; Gaps 0
OY	1 MNPNRSEHDITKTENNENVTNHNQVPLAEIPNPFLIEDLNKKEFLRMADNTTEALDSS 60
DB	1 MNPNRSEHDITKTENNENVTNHNQVPLAEIPNPFLIEDLNKKEFLRMADNTTEALDSS 60
OY	61 TTKDVIOKGISVVGDLIGVGFEPFGALVSFTYNFINTIMPSEDPPKAFMEGYEALMDOK 120
DB	61 TTKDVIOKGISVVGDLIGVGFEPFGALVSFTYNFINTIMPSEDPPKAFMEGYEALMDOK 120
OY	121 IADYANKKLAELQGONNVEDVYSLSSMOKKPVRSDPHSGRIRELFSQAESHFRNS 180
DB	121 IADYANKKLAELQGONNVEDVYSLSSMOKKPVRSDPHSGRIRELFSQAESHFRNS 180
OY	181 MPSEFAISGEVLEFLTYYAQAANTHLELKLDAQIYGEGMEGKEKDIAEFYKKRLKLTQEYT 240
DB	181 MPSEFAISGEVLEFLTYYAQAANTHLELKLDAQIYGEGMEGKEKDIAEFYKKRLKLTQEYT 240
OY	241 DHCVKMYNWGLDKLRGSYSSESVNENRRREMTLYVLDLIALFPDYVRLRYEKVEYTELT 300
DB	241 DHCVKMYNWGLDKLRGSYSSESVNENRRREMTLYVLDLIALFPDYVRLRYEKVEYTELT 300
OY	301 RDVLTDPITYGVNNLRKGTTFESNIENYIRKPHLFIDLHRIQHTRPQGYGGDSFNMYMS 360
DB	301 RDVLTDPITYGVNNLRKGTTFESNIENYIRKPHLFIDLHRIQHTRPQGYGGDSFNMYMS 360
OY	361 GNIVSTRPISIGSNDITTSPEYGRKSSBPVNOLFENGEKYRAVAANTNLAVMPASVYSGVT 420
DB	361 GNIVSTRPISIGSNDITTSPEYGRKSSBPVNOLFENGEKYRAVAANTNLAVMPASVYSGVT 420
OY	421 KVEFSQYNDOTDEASTQTYSKRNAGVASWDSIDQLPPEYTDDEPLEKGYSHOLNYWCFL 480
DB	421 KVEFSQYNDOTDEASTQTYSKRNAGVASWDSIDQLPPEYTDDEPLEKGYSHOLNYWCFL 480
OY	481 MOSSRGIPVLTMYTHHSVDFFNMIDSKTIQLPLVKRYKILQSAGSYVAGRFPGGDITIOC 540
DB	481 MOSSRGIPVLTMYTHHSVDFFNMIDSKTIQLPLVKRYKILQSAGSYVAGRFPGGDITIOC 540

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OY 541 TNGSAAATVYVPDVSYSQKVRARHXYASTSITFTLSLDGAPFNQYFDDKTIKNGDILT 600
DB 541 TNGSAAATVYVPDVSYSQKVRARHXYASTSITFTLSLDGAPFNQYFDDKTIKNGDILT 600
OY 601 YNSFNLASFTPELPGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFTPELPGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
RESULT 12
AAW34829
ID AAW34829 standard: Protein: 644 AA.
XX
AC AAW34829:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein S449A.
XX
OS CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX increased toxicity; Coleopteran insect; Colorado potato beetle;
XX relative solvent accessibility; plant resistance;
XX Diabrotica virgifera virgifera.
XX Synthetic.
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 449 /label= S449A
FT /note= "wild type Ser replaced with Ala"
FT
PN US5659123-A.
XX
PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI Jansens S, Peteroen M, Van Rie J;
XX WPT, 1997-424316/39.
XX
PT Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40% or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 7.12 microgram per millilitre, compared to 4.04 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA:

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Best Local Similarity 99.8%; Pred. No. 2.9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TTKDYIOGISVGDLLGVGPPGALVSEFYNTFLTIMPSEDPWKAEMEYVETALMDOK 120
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DB 241 DHCKWYNVGLDKRGSSYSESWNFNRYRREMTLTVLDLALPLDYRLYPREVKTELT 300
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DB 361 GNYVSTRPSIGSNDIITSPYGNKSSPEVONLEFNCKEYRAVANNTLAWPSAVYSGVT 420
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DB 481 MGSRGITPVLWTHTKSVDFEFNNIDSKKITQPLVKAAYKLGASVAVAGPRTGGDIIOC 540
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DB 601 YNSFNLFASFPELSEGNNOIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 13
AAM34841
ID AAM34841 standard; Protein; 644 AA.
XX
AC AAM34841;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein S442A.
XX
KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 442 /Label= S442A
FT /note= "wild type Ser replaced with Ala"
XX
XX US5659123-A.

```

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PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLB2) PLANT GENETIC SYSTEMS NV.
XX
PI Jansens S, Peferoen M, Van Rie J;
XX WPI; 1997-424316/39.
XX
DR Modified Bacillus thuringiensis CryIIA proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
PS Claim 9; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested, and the present mutant protein was
CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
CC toxicity of the mutant protein for this Diabrotica pest was
CC significantly below the toxicity of the native CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA;
XX
Query Match 99.9%; Score 3403; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 2.9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MNPNNRSEHDITKTENNEVPNNHVOYPLAETPPTLEDLNYKFEFLMTADNTEALDSS 60
QY 61 TTKDYIOGISVGDLLGVGPPGALVSEFYNTFLTIMPSEDPWKAEMEYVETALMDOK 120
DB 61 TTKDYIOGISVGDLLGVGPPGALVSEFYNTFLTIMPSEDPWKAEMEYVETALMDOK 120
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DB 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIRLELSQAESHFRNS 180
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DB 361 GNYVSTRPSIGSNDIITSPYGNKSSPEVONLEFNCKEYRAVANNTLAWPSAVYSGVT 420
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DB 421 KVERSOYNDQDEASTQYDSKRNKGVASWDSIDQLEPPTTDEPLEKGYSHOANTYMCFL 480

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 QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 14
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 ID AAM34822 standard; Protein; 644 AA.
 AC AAM34822;
 XX
 DT 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein V311A.
 XX
 KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 311 /label= V311A
 FT /note= "wild type Val replaced with Ala"

US5659123-A.
 PD 19-AUG-1997.
 XX
 PD 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 XX
 DR WPI; 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1; Page -; 22pp; English.
 XX
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.09 microgram per millilitre, compared to 1.21 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created

CC using information provided.
 XX
 SQ Sequence 644 AA;
 Query Match 99.9%; Score 3402; DB 18; Length 644;
 Best local similarity 99.8%; Pred. No. 3.5e-268;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 541 TENGSAATITVTPDVYSQKRYARIRHYASTSQITFTLSLDGAPFNOYFDTINKGDTLT 600
 QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 15
 AAM34828
 ID AAM34828 standard; Protein; 644 AA.
 AC AAM34828;
 XX
 DT 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein V448A.
 XX
 KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 448

FT /label- V448A
 /note- "wild type Val replaced with Ala"
 XX US659123-A.
 PN 19-AUG-1997.
 PD 19-AUG-1997.
 XX 26-AUG-1994: 94US-0295060.
 XX 26-AUG-1994: 94US-0295060.
 XX 26-AUG-1994: 94US-0295060.
 XX (PLB2) PLANT GENETIC SYSTEMS NV.
 PA Janssens S, Peferoen M, Van Rie J;
 PI WPI; 1997-424316/39.
 DR Modified Bacillus thuringiensis CryIII proteins - with increased
 XX toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 XX Example 1: Page -: 22pp; English.
 PS
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 11.52 microgram per millilitre, compared to 4.04 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 XX
 SQ Sequence 644 AA;
 Query Match 99.9%; Score 3402; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 3.5e-268;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNPNNSEHDTIKTTEENNEPTNHNVOYPLAETNPTELDLNTKEFLRMTADNNTTEALDSS 60
 DB 1 MNPNNSEHDTIKTTEENNEPTNHNVOYPLAETNPTELDLNTKEFLRMTADNNTTEALDSS 60
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DB 361 GNVSTRPSIGSNDITSPFYGNKSSEPVQNLFEENGKEYRAVANTNLAWPSAVYSGVT 420
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 DB 541 TENGSAATYVTPDVYSQKYPARIRHYASTSQITFTLSIDGAPFNQYFDTKINKG 600
 QY 601 YNSFNLSFSTPELGSNNLQIGVTGLSGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLSFSTPELGSNNLQIGVTGLSGDKVYIDKIEFIPVN 644

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 Job time : 41 secs

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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:05:49 ; Search time 16 Seconds

(without alignments)
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Title: US-09-943-692-2

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Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3406	100.0	644	1 US-08-072-281-2	Sequence 2, Appl
3	3406	100.0	644	1 US-08-293-060-2	Sequence 2, Appl
4	3406	100.0	644	1 US-08-759-446-2	Sequence 2, Appl
5	3406	100.0	644	4 US-09-027-998A-2	Sequence 2, Appl
6	3406	100.0	644	5 PCT-US92-11337-4	Sequence 4, Appl
7	3406	100.0	652	3 US-08-996-441B-113	Sequence 113, App
8	3406	100.0	652	3 US-08-993-722A-113	Sequence 113, App
9	3406	100.0	652	3 US-08-993-170A-113	Sequence 113, App
10	3406	100.0	652	3 US-08-993-775B-113	Sequence 113, App
11	3328	97.7	645	1 US-08-293-060-4	Sequence 4, Appl
12	3149	92.5	597	1 US-08-704-966-2	Sequence 2, Appl
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14	3144	92.3	610	3 US-08-704-966-4	Sequence 4, Appl
15	3144	92.3	610	3 US-08-705-438-4	Sequence 4, Appl
16	2564.5	75.3	649	3 US-08-996-441B-109	Sequence 109, App
17	2564.5	75.3	649	3 US-08-993-722A-109	Sequence 109, App
18	2564.5	75.3	649	3 US-08-993-170A-109	Sequence 109, App
19	2564.5	75.3	649	3 US-08-993-775B-109	Sequence 109, App
20	2383	70.0	651	3 US-08-996-441B-56	Sequence 56, Appl
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25	2378.5	69.8	652	3 US-08-993-722A-50	Sequence 50, Appl
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27	2378.5	69.8	652	3 US-08-993-775B-50	Sequence 50, Appl

28	2369.5	69.6	652	3 US-08-996-441B-46	Sequence 46, Appl
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31	2369.5	69.6	652	3 US-08-993-775B-46	Sequence 46, Appl
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36	2350.5	69.0	652	3 US-08-996-441B-48	Sequence 48, Appl
37	2350.5	69.0	652	3 US-08-993-722A-48	Sequence 48, Appl
38	2350.5	69.0	652	3 US-08-993-170A-48	Sequence 48, Appl
39	2350.5	69.0	652	3 US-08-993-775B-48	Sequence 48, Appl
40	2349.5	69.0	652	3 US-08-996-441B-54	Sequence 54, Appl
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44	2348.5	69.0	652	3 US-08-996-441B-44	Sequence 44, Appl
45	2348.5	69.0	652	3 US-08-993-722A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-07-828-788A-4
Sequence 4, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGRIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF FRANK GARTNER
CLONE: 40D1
US-07-828-788A-4

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDITKTENNENVPNNVOYPLAETPNPTLEDLNKKEFLMTADNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNNVOYPLAETPNPTLEDLNKKEFLMTADNTEALDSS 60
QY 61 TTKDVIOKGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
DB 61 TTKDVIOKGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
QY 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
DB 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
QY 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
DB 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
QY 301 RDVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLHRIQFHTRPQGYGNDSEFNWS 360
DB 301 RDVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLHRIQFHTRPQGYGNDSEFNWS 360
QY 361 GNYVSTRPSISGNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSISGNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
QY 421 KVEFSQYNDOTDEASTQYDSKRNAGVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCL 480
DB 421 KVEFSQYNDOTDEASTQYDSKRNAGVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCL 480
QY 481 MOSRGITPVLTWTHKSVDFNMDSKKITQOLPLVAKYKLGASAVYAGPRFTGGDIIOC 540
DB 481 MOSRGITPVLTWTHKSVDFNMDSKKITQOLPLVAKYKLGASAVYAGPRFTGGDIIOC 540
QY 541 TENGSAATIVTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
DB 541 TENGSAATIVTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNLASSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPIVN 644
DB 601 YNSFNLASSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPIVN 644

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RESULT 2

US-08-072-281-2
 Sequence 2, Application US/08072281
 Patent No. 5495071

GENERAL INFORMATION:

APPLICANT: Fischhoff, David A.

APPLICANT: Fuchs, Roy L.

APPLICANT: Lawrik, Paul B.

APPLICANT: McPherson, Sylvia A.

APPLICANT: Perlak, Frederick J.

TITLE OF INVENTION: Insect Resistant Plants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Lawrence M. Lavin, Jr., Monsanto Co., BB4F

STREET: 700 Chesterfield Parkway No. 5495071th

CITY: St. Louis

STATE: Missouri

COUNTRY: United States of America

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/072,281
 FILING DATE: 19930604
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/533284
 FILING DATE: 14-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Lavin Jr., Lawrence M.
 REGISTRATION NUMBER: 30,768
 REFERENCE/DOCKET NUMBER: 38-21(10629)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 537-7286
 TELEFAX: (314) 537-6047
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 644 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDITKTENNENVPNNVOYPLAETPNPTLEDLNKKEFLMTADNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNNVOYPLAETPNPTLEDLNKKEFLMTADNTEALDSS 60
QY 61 TTKDVIOKGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
DB 61 TTKDVIOKGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
QY 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
DB 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
QY 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
DB 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
QY 301 RDVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLHRIQFHTRPQGYGNDSEFNWS 360
DB 301 RDVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLHRIQFHTRPQGYGNDSEFNWS 360
QY 361 GNYVSTRPSISGNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSISGNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
QY 421 KVEFSQYNDOTDEASTQYDSKRNAGVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCL 480
DB 421 KVEFSQYNDOTDEASTQYDSKRNAGVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCL 480
QY 481 MOSRGITPVLTWTHKSVDFNMDSKKITQOLPLVAKYKLGASAVYAGPRFTGGDIIOC 540
DB 481 MOSRGITPVLTWTHKSVDFNMDSKKITQOLPLVAKYKLGASAVYAGPRFTGGDIIOC 540
QY 541 TENGSAATIVTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
DB 541 TENGSAATIVTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNLASSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPIVN 644
DB 601 YNSFNLASSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPIVN 644

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RESULT 3

US-08-295-060-2
 : Sequence 2, Application US/08295060
 : Patent No. 5659123
 : GENERAL INFORMATION:
 : APPLICANT: VAN RIE, Jeroen
 : APPLICANT: JANSSEN, Stefan
 : APPLICANT: PERFEROEN, Marjolix
 : TITLE OF INVENTION: NEW DIABROTICA TOXINS
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Burns, Doane, Swecker & Matchis
 : STREET: P.O. Box 1404
 : CITY: Alexandria
 : STATE: Virginia
 : COUNTRY: United States
 : ZIP: 22133-1404
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/295,060
 : FILING DATE: 26-AUG-1994
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Crane-Feurly, Sharon E
 : REGISTRATION NUMBER: 36,113
 : REFERENCE/DOCKET NUMBER: 010830-052
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 836-6620
 : TELEFAX: (703) 836-6620
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-295-060-2

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7.1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPNPTLEDINTYKEFLRMATDNNTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPNPTLEDINTYKEFLRMATDNNTEALDSS 60
 QY 61 TTAKVIOKGISVVDLLGVGFPFGGALVSYFTNFMTNPSEDPKMAFMEQVEALMDOK 120
 DB 61 TTAKVIOKGISVVDLLGVGFPFGGALVSYFTNFMTNPSEDPKMAFMEQVEALMDOK 120
 QY 121 IADYAKKKAALAEGLGNVEDYSAVSMOKNPVSSRNPHSOGRIEELSOASHEFRNS 180
 DB 121 IADYAKKKAALAEGLGNVEDYSAVSMOKNPVSSRNPHSOGRIEELSOASHEFRNS 180
 QY 181 MPFAISGEYVLFITYAQAANTHILFLKDAQIYGEEMGYEKEDIAEFYKROKLTQOET 240
 DB 181 MPFAISGEYVLFITYAQAANTHILFLKDAQIYGEEMGYEKEDIAEFYKROKLTQOET 240
 QY 241 DHCVKMYNVGLDKLGRSSYESSWVFNRRRMTLTVDLALFPLDYVRLYPKVEKTELT 300
 DB 241 DHCVKMYNVGLDKLGRSSYESSWVFNRRRMTLTVDLALFPLDYVRLYPKVEKTELT 300
 QY 301 RDVLTDPVGVNRLRGYGTSTNENTYRKPHLFDYLRHIOFHRFOPGVYGNDSFNWMS 360
 DB 301 RDVLTDPVGVNRLRGYGTSTNENTYRKPHLFDYLRHIOFHRFOPGVYGNDSFNWMS 360
 QY 361 GNYVSTRSISNDITSPFYGNKSSSEPVQNLFEFGKEVYRAVANTNLAVPSSAVYSQVT 420
 DB 361 GNYVSTRSISNDITSPFYGNKSSSEPVQNLFEFGKEVYRAVANTNLAVPSSAVYSQVT 420
 QY 421 KVESQYNDQIDEASTQTYDSKRNKAVSWDSIDQLPETTDEPLEKGYSHQNLVWCF 480

US-08-759-446-2
 : Sequence 2, Application US/08759446
 : Patent No. 5763241
 : GENERAL INFORMATION:
 : APPLICANT: Fischhoff, David A.
 : APPLICANT: Fuchs, Roy L.
 : APPLICANT: Lavrik, Paul B.
 : APPLICANT: McPherson, Sylvia A.
 : TITLE OF INVENTION: Insect Resistant Plants
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lawrence M. Lavlin, Jr., Monsanto Co., BBAF
 : STREET: 700 Chesterfield Parkway No. 5763241ch
 : CITY: St. Louis
 : STATE: Missouri
 : COUNTRY: United States of America
 : ZIP: 63198
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/759,446
 : FILING DATE: 05-DEC-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/072,281
 : FILING DATE:
 : APPLICATION NUMBER: US 07/523284
 : FILING DATE: 14-MAY-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lavlin Jr., Lawrence M.
 : REGISTRATION NUMBER: 30,768
 : REFERENCE/DOCKET NUMBER: 38-21(10629)A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314) 537-7286
 : TELEFAX: (314) 537-6047
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-759-446-2

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7.1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPNPTLEDINTYKEFLRMATDNNTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPNPTLEDINTYKEFLRMATDNNTEALDSS 60
 QY 61 TTAKVIOKGISVVDLLGVGFPFGGALVSYFTNFMTNPSEDPKMAFMEQVEALMDOK 120

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 644 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: US-09-027-998A-2

Query Match 100.0%; Score 3406; Db 4; Length 644;
Best Local Similarity 100.0%; Prid. No. 7.1e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 MNPNRSEHDTIKTTENNEVPTNHNQYLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
Db 1 MNPNRSEHDTIKTTENNEVPTNHNQYLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60

QY 61 TTKDVIQGISVYGDLLGVGPFEGGALVSEYTFNPLNTIMPSSEDPMKAFMEQYBALDOK 120
Db 61 TTKDVIQGISVYGDLLGVGPFEGGALVSEYTFNPLNTIMPSSEDPMKAFMEQYBALDOK 120

QY 121 IADYKKNKALAELOGLQNNVEDYSAISSWQKNVSSNPNRSGQRIRLETLSQASHRRNS 180
Db 121 IADYKKNKALAELOGLQNNVEDYSAISSWQKNVSSNPNRSGQRIRLETLSQASHRRNS 180

QY 181 MPFASISGEVLFITTYAQAAANTHLFLKDAQIYGEWGEKEKEDIAEFYRKQLTQEYT 240
Db 181 MPFASISGEVLFITTYAQAAANTHLFLKDAQIYGEWGEKEKEDIAEFYRKQLTQEYT 240

QY 241 DHCYKYNVNGLDKLRGSSYESMVNENRIRREMTLTVLDLAFPLVYRRLYPREVKTLELT 300
Db 241 DHCYKYNVNGLDKLRGSSYESMVNENRIRREMTLTVLDLAFPLVYRRLYPREVKTLELT 300

QY 301 RDVLTPDIVGVNNLRGYSYGTTFNSIENTYIRKPHLEPDLYLRHIOFHTRFOPGYYGNDSEFWYMS 360
Db 301 RDVLTPDIVGVNNLRGYSYGTTFNSIENTYIRKPHLEPDLYLRHIOFHTRFOPGYYGNDSEFWYMS 360

QY 361 GNYVSTRPISNDIITSPFYGKNSSEPVQYLENGEKYRVAANTMLAWPSAVYSGVT 420
Db 361 GNYVSTRPISNDIITSPFYGKNSSEPVQYLENGEKYRVAANTMLAWPSAVYSGVT 420

QY 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSMDSIDQLPETTDEBLEKGYSHQINTYWCFL 480
Db 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSMDSIDQLPETTDEBLEKGYSHQINTYWCFL 480

QY 481 MGSNGTIPVLTWKHSYDVFNMIDSKKTIQLPLVKAYKLOSQSVYAGRFPGGDIIOC 540
Db 481 MGSNGTIPVLTWKHSYDVFNMIDSKKTIQLPLVKAYKLOSQSVYAGRFPGGDIIOC 540

QY 541 TENGSAATIVTTPVYSQKRIARIHASTSQTFFTLSLGAPFNQYFPDKTINKGDTLT 600
Db 541 TENGSAATIVTTPVYSQKRIARIHASTSQTFFTLSLGAPFNQYFPDKTINKGDTLT 600

QY 601 YNSFNLASFTPELSCNNLIQVTLGSAGDKYIDKIEFIPVN 644
Db 601 YNSFNLASFTPELSCNNLIQVTLGSAGDKYIDKIEFIPVN 644

RESULT 6
PCT-US92-11337-4
Sequence 4, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIMANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/11337
 FILING DATE: 19921231
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 97/828,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: SALIVANCHIK, DAVID R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA75
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-372-5800
 TELEFAX: 904-375-8100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 644 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: BACILLUS THURINGIENSIS
 STRAIN: NIGERIENSIS
 INDIVIDUAL ISOLATE: PS40D1
 IMMEDIATE SOURCE:
 LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF FRANK GAERTNER
 CLONE: 40D1
 PCT-US92-11337-4

Query Match 100.0%; Score 3406; DB 5; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7.1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDNTKEFLRMTADNTEALDSS 60
 DB 1 MNPNNSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDNTKEFLRMTADNTEALDSS 60
 QY 61 TTKDVIOKGSIVGDLGVGPFPGALVSFTYNTFNTIMPSEDPMKAFMEOVEALMDOK 120
 DB 61 TTKDVIOKGSIVGDLGVGPFPGALVSFTYNTFNTIMPSEDPMKAFMEOVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180
 DB 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180
 QY 181 MPSPAIISGYEVLFTTYAQAANTHPLFLKPAQITGEEMGKEKEDIAEFYRQKLIOEYT 240
 DB 181 MPSPAIISGYEVLFTTYAQAANTHPLFLKPAQITGEEMGKEKEDIAEFYRQKLIOEYT 240
 QY 241 DHCKWYNVGLDKLGRSSYSWVNFNRYRREMTLTVLDLALPFLYDRLVYPRKEVTELT 300
 DB 241 DHCKWYNVGLDKLGRSSYSWVNFNRYRREMTLTVLDLALPFLYDRLVYPRKEVTELT 300
 QY 301 RDVLTDPIVGNVNLRGYGTTFSTNENYIRKPHLPDYLRHIOFHTRFQPGYGGNDSFVWS 360
 DB 301 RDVLTDPIVGNVNLRGYGTTFSTNENYIRKPHLPDYLRHIOFHTRFQPGYGGNDSFVWS 360
 QY 361 GNYSTRISGNDITSPFGKNSSEPVONLEFNGEKKYRAVANTMLAVPSPAVSGVT 420
 DB 361 GNYSTRISGNDITSPFGKNSSEPVONLEFNGEKKYRAVANTMLAVPSPAVSGVT 420
 QY 421 KVEFSQYNDQDEASTQYYSKRNAGVSWDSIDQLPEPTTDEPLEKYSQOLNVMCF 480
 DB 421 KVEFSQYNDQDEASTQYYSKRNAGVSWDSIDQLPEPTTDEPLEKYSQOLNVMCF 480
 QY 481 MGSNGTIPVLTWHKSVDFNMIDSKKITQPLVYKAVKLGSGSVAVAGPFTGGDIQC 540

DB 481 MGSNGTIPVLTWHKSVDFNMIDSKKITQPLVYKAVKLGSGSVAVAGPFTGGDIQC 540
 QY 541 TENGSAATVTPVVSQKRAIRHYASTSOIFETLSLDCAPNOYFPKTIKGTLT 600
 DB 541 TENGSAATVTPVVSQKRAIRHYASTSOIFETLSLDCAPNOYFPKTIKGTLT 600
 QY 601 YNSFNIASTPTELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNIASTPTELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

RESULT 7
 US-08-996-441B-113
 Sequence 113, Application US/08996441B
 Patent No. 6023013

GENERAL INFORMATION:
 APPLICANT: English, Leigh H.
 APPLICANT: Brusock, Susan M.
 APPLICANT: Malvar, Thomas M.
 APPLICANT: Bryson, James W.
 APPLICANT: Kulesza, Caroline A.
 APPLICANT: Walters, Frederick S.
 APPLICANT: Slatin, Stephen L.
 APPLICANT: Von Tersch, Michael A.
 APPLICANT: Romano, Charles
 TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,441B
 FILING DATE: 18-DEC-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MECO:151
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 652 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-996-441B-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
 Best Local Similarity 100.0%; Pred. No. 7.2e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDNTKEFLRMTADNTEALDSS 60
 DB 9 MNPNNSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDNTKEFLRMTADNTEALDSS 68
 QY 61 TTKDVIOKGSIVGDLGVGPFPGALVSFTYNTFNTIMPSEDPMKAFMEOVEALMDOK 120
 DB 61 TTKDVIOKGSIVGDLGVGPFPGALVSFTYNTFNTIMPSEDPMKAFMEOVEALMDOK 128
 QY 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180

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Db 129 IADYAKKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSGRIRELPSQASHFRNS 188
QY 181 MPSFAISGEVLEFLTTAAQANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOET 240
Db 189 MPSFAISGEVLEFLTTAAQANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOET 248
QY 241 DHCVKWYNGVGLDKLRSSSVESWVNFNRKREMTLVLDLALFPLDVRILYPREVTELT 300
Db 249 DHCVKWYNGVGLDKLRSSSVESWVNFNRKREMTLVLDLALFPLDVRILYPREVTELT 308
QY 301 RDVLTDPYGVNNLRGCTTFSENIENYIRKPHLFDYLRHIOFHTROPQYGNDSFNWMS 360
Db 309 RDVLTDPYGVNNLRGCTTFSENIENYIRKPHLFDYLRHIOFHTROPQYGNDSFNWMS 368
QY 361 GNVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Db 369 GNVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCEFL 480
Db 429 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCEFL 488
QY 481 MGSRGITPVLTTWTHKSVDFNNMIDSKKITQLPLVKAAYKLQSGASVYAGPRTGGDIIOC 540
Db 489 MGSRGITPVLTTWTHKSVDFNNMIDSKKITQLPLVKAAYKLQSGASVYAGPRTGGDIIOC 548
QY 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 600
Db 549 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 608
QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPIVN 644
Db 609 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPIVN 652

```

RESULT 8
US-08-993-722A-113
; Sequence 113, Application US/08993722A
; Patent No. 6060594

GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 512/418-3106
; FAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-993-722A-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNRSEHDITKTENNEVPNTNVOPLATPMTLEDLNYKFEFLMTADNNTALDSS 60
Db 9 MNPNRSEHDITKTENNEVPNTNVOPLATPMTLEDLNYKFEFLMTADNNTALDSS 68
QY 61 TTKDVIQGISVGDLLGVGFPGALVSEFTNLTIMPSEDPMKAFMEQVEALMDOK 120
Db 69 TTKDVIQGISVGDLLGVGFPGALVSEFTNLTIMPSEDPMKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSGRIRELPSQASHFRNS 180
Db 129 IADYAKKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSGRIRELPSQASHFRNS 188
QY 181 MPSFAISGEVLEFLTTAAQANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOET 240
Db 189 MPSFAISGEVLEFLTTAAQANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOET 248
QY 241 DHCVKWYNGVGLDKLRSSSVESWVNFNRKREMTLVLDLALFPLDVRILYPREVTELT 300
Db 249 DHCVKWYNGVGLDKLRSSSVESWVNFNRKREMTLVLDLALFPLDVRILYPREVTELT 308
QY 301 RDVLTDPYGVNNLRGCTTFSENIENYIRKPHLFDYLRHIOFHTROPQYGNDSFNWMS 360
Db 309 RDVLTDPYGVNNLRGCTTFSENIENYIRKPHLFDYLRHIOFHTROPQYGNDSFNWMS 368
QY 361 GNVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Db 369 GNVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCEFL 480
Db 429 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCEFL 488
QY 481 MGSRGITPVLTTWTHKSVDFNNMIDSKKITQLPLVKAAYKLQSGASVYAGPRTGGDIIOC 540
Db 489 MGSRGITPVLTTWTHKSVDFNNMIDSKKITQLPLVKAAYKLQSGASVYAGPRTGGDIIOC 548
QY 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 600
Db 549 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 608
QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPIVN 644
Db 609 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPIVN 652

```

RESULT 9
US-08-993-170A-113
; Sequence 113, Application US/08993170A
; Patent No. 6063597

GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO

TITLE OF INVENTION: COLEOPTERAN INSECTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS: 113
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.170A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-170A-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNNNSEHDTITKTENNEVPNTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
DB 9 MNNNNSEHDTITKTENNEVPNTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 68
QY 61 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTFLNTIWPSEDPMKAFMEQVEALMDOK 120
DB 69 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTFLNTIWPSEDPMKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRTRELSQAESHFRNS 180
DB 129 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRTRELSQAESHFRNS 188
QY 181 MPFAISGYEVLFTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 189 MPFAISGYEVLFTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 248
QY 241 DHCKYKYNVGLDKRGSSYSWVFNRYRREMTLTVDLALPPLYVRYLPKEVTELT 300
DB 249 DHCKYKYNVGLDKRGSSYSWVFNRYRREMTLTVDLALPPLYVRYLPKEVTELT 308
QY 301 RDVLTIDYVGNNGRGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQPGYTGNDSEFNYS 360
DB 309 RDVLTIDYVGNNGRGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQPGYTGNDSEFNYS 368
QY 361 GNYVSTRPISGSDIITSPYGNKSSPPVONLEFNGEKRYRAVANINLAWPASVYSGVT 420
DB 369 GNYVSTRPISGSDIITSPYGNKSSPPVONLEFNGEKRYRAVANINLAWPASVYSGVT 428
QY 421 KVESQVNDQDEASTQTYOSKRNAGVAVSMDSIDOLPETTDEPLEKGYSHQLNVCFL 480
DB 429 KVESQVNDQDEASTQTYOSKRNAGVAVSMDSIDOLPETTDEPLEKGYSHQLNVCFL 488
QY 481 MGSRGITPVLWTJHKSVDFFNMIDSKKITQPLVKAYKLOSASVYVAGPRFTGGDITQC 540
DB 489 MGSRGITPVLWTJHKSVDFFNMIDSKKITQPLVKAYKLOSASVYVAGPRFTGGDITQC 548

QY 541 TENGSAATIVYTPDVSYSQKRYARIHYASTQITFTLSDGAPPNOYFENKTIKNGDTLT 600
DB 549 TENGSAATIVYTPDVSYSQKRYARIHYASTQITFTLSDGAPPNOYFENKTIKNGDTLT 608
QY 601 YNSFNILASFSPFELSGNNLQIGVTGLSAGDKYIDNIEFIPVN 644
DB 609 YNSFNILASFSPFELSGNNLQIGVTGLSAGDKYIDNIEFIPVN 652

RESULT 10
US-08-993-775B-113
Sequence 113, Application US/08993775B
Patent No. 6077824
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brunsack, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terach, Michael A.
TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.775B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-775B-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNNNSEHDTITKTENNEVPNTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
DB 9 MNNNNSEHDTITKTENNEVPNTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 68
QY 61 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTFLNTIWPSEDPMKAFMEQVEALMDOK 120
DB 69 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTFLNTIWPSEDPMKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRTRELSQAESHFRNS 180
DB 129 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRTRELSQAESHFRNS 188
QY 181 MPFAISGYEVLFTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240

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Db 189 MFPSALSGEVLFTTYAQAANTHLFLKDAQYGEEMGEKEDIAEFKROLKTOEY 248
QY 241 DHCWYNNGLDKLGRSSYSEWVNNRIRREMTLVLDLIALFPLDYVLYPEVTELT 300
Db 249 DHCWYNNGLDKLGRSSYSEWVNNRIRREMTLVLDLIALFPLDYVLYPEVTELT 308
QY 301 RDVLTDPYGVNNLRGYGTFPSNIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 360
Db 309 RDVLTDPYGVNNLRGYGTFPSNIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 368
QY 361 GNVSTRPSIGSNDITSPFYGNKSEPPQNLFEENGEKYRAVANTNLAWPSAYSGVT 420
Db 369 GNVSTRPSIGSNDITSPFYGNKSEPPQNLFEENGEKYRAVANTNLAWPSAYSGVT 428
QY 421 KVEFSQNDOTDEASTQYDYSKRNGAVSMDSIDQLPEPTTDEPLEKGSQHLNVMCTL 480
Db 429 KVEFSQNDOTDEASTQYDYSKRNGAVSMDSIDQLPEPTTDEPLEKGSQHLNVMCTL 488
QY 481 MGSRTIPLVLTWTHKSVDFNNMIDSKITQLPLVKAAYLQSGASVAGPRTGGDIQC 540
Db 489 MGSRTIPLVLTWTHKSVDFNNMIDSKITQLPLVKAAYLQSGASVAGPRTGGDIQC 548
QY 541 TENGSAATIVYTPDVSQKRYARIRHYASTSQTFTLSLDGAPFNOYFDDKTKNGDITL 600
Db 549 TENGSAATIVYTPDVSQKRYARIRHYASTSQTFTLSLDGAPFNOYFDDKTKNGDITL 608
QY 601 YNSFNLASSTPELSCNNLQIGVTGLSAGDKVYIDKIEFLPVN 644
Db 609 YNSFNLASSTPELSCNNLQIGVTGLSAGDKVYIDKIEFLPVN 652

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RESULT 11

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US-08-295-060-4
; Sequence 4, Application US/08295060
; Patent No. 5659123

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GENERAL INFORMATION:

```

; APPLICANT: VAN RIE, Jeroen
; APPLICANT: JANSSENS, Stefan
; APPLICANT: PERPEROEN, Marilix
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:

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SEQUENCE CHARACTERISTICS:

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; LENGTH: 645 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; US-08-295-060-4

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Query Match 97.7%; Score 3328; DB 1; Length 645;
Best Local Similarity 98.6%; Pred. No. 2,4e-270;
Matches 634; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 2 NPNNSEHDITKTENNBNVPTNNHVOYPLAETPNPTLEDNANKELRMADNNTALDSSST 61
Db 3 NPNNSEHDITKTENNBNVPTNNHVOYPLAETPNPTLEDNANKELRMADNNTALDSSST 62
QY 62 TKDVIQKISVVGDLIGVGFPEFGALVSFTYNTLNTIWPSEDPWKAAMEQVEALMDOKI 121
Db 63 TKDVIQKISVVGDLIGVGFPEFGALVSFTYNTLNTIWPSEDPWKAAMEQVEALMDOKI 122
QY 122 ADVAKNKALAELOGLONNVEDYVSAISWQKNPVSSRNPHSQGIRLFSQASHFENSM 181
Db 123 ADVAKNKALAELOGLONNVEDYVSAISWQKNPVSSRNPHSQGIRLFSQASHFENSM 182
QY 182 PSFALSGEVLFTTYAQAANTHLFLKDAQYGEEMGEKEDIAEFKROLKTOEYTD 241
Db 183 PSFALSGEVLFTTYAQAANTHLFLKDAQYGEEMGEKEDIAEFKROLKTOEYTD 242
QY 242 HCWYNNGLDKLGRSSYSEWVNNRIRREMTLVLDLIALFPLDYVRLYPKVEKTELTR 301
Db 243 HCWYNNGLDKLGRSSYSEWVNNRIRREMTLVLDLIALFPLDYVRLYPKVEKTELTR 302
QY 302 DVLTDPIYGVNNLRGYGTFPSNIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 361
Db 303 DVLTDPIYGVNNLRGYGTFPSNIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 362
QY 362 NYVSTRPSIGSNDITSPFYGNKSEPPQNLFEENGEKYRAVANTNLAWPSAYSGVT 421
Db 363 NYVSTRPSIGSNDITSPFYGNKSEPPQNLFEENGEKYRAVANTNLAWPSAYSGVT 422
QY 422 VEFQYNDOTDEASTQYDYSKRNGAVSMDSIDQLPEPTTDEPLEKGSQHLNVMCTL 481
Db 423 VEFQYNDOTDEASTQYDYSKRNGAVSMDSIDQLPEPTTDEPLEKGSQHLNVMCTL 482
QY 482 QGSRGTIPLVLTWTHKSVDFNNMIDSKITQLPLVKAAYLQSGASVAGPRTGGDIQC 541
Db 483 QGSRGTIPLVLTWTHKSVDFNNMIDSKITQLPLVKAAYLQSGASVAGPRTGGDIQC 542
QY 542 ENGSAATIVYTPDVSQKRYARIRHYASTSQTFTLSLDGAPFNOYFDDKTKNGDITLY 601
Db 543 ENGSAATIVYTPDVSQKRYARIRHYASTSQTFTLSLDGAPFNOYFDDKTKNGDITLY 602
QY 602 NSFNLASSTPELSCNNLQIGVTGLSAGDKVYIDKIEFLPVN 644
Db 603 NSFNLASSTPELSCNNLQIGVTGLSAGDKVYIDKIEFLPVN 645

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RESULT 12

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US-08-704-966-2
; Sequence 2, Application US/08704966
; Patent No. 6013523

```

GENERAL INFORMATION:

```

; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801

```

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,966
FILING DATE: 29-AUG-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
FILING DATE: 09-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-966-2

Query Match 92.5%; Score 3149; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.1e-255;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALSDSTTKDVYKIGISVVDLGVGFPFGALVSPYTNFLNTIMPSEDPMK 107
DB 1 MTADNNTALSDSTTKDVYKIGISVVDLGVGFPFGALVSPYTNFLNTIMPSEDPMK 60

QY 108 AFMEQVALMDOKIADYAKKALAELOGIANNEDVYSAISSWQKNPVSSRNHSGRR 167
DB 61 AFMEQVALMDOKIADYAKKALAELOGIANNEDVYSAISSWQKNPVSSRNHSGRR 120

QY 168 ELFSQASHFRNSMPSFAISGEYVFLTYTAAANTHLFLKDAQIYGEEMGEKEDIAE 227
DB 121 ELFSQASHFRNSMPSFAISGEYVFLTYTAAANTHLFLKDAQIYGEEMGEKEDIAE 180

QY 228 FYKROLKLTQETDHCYKWNVGLDKLRGSSYESWVFNRYRREMLTVLDIALPFLYD 287
DB 181 FYKROLKLTQETDHCYKWNVGLDKLRGSSYESWVFNRYRREMLTVLDIALPFLYD 240

QY 288 VRLPKKEVKELTDVLDPLVGNVNNRGYTTSENIENTIRKHLDDYLRHIOFHRFQ 347
DB 241 VRLPKKEVKELTDVLDPLVGNVNNRGYTTSENIENTIRKHLDDYLRHIOFHRFQ 300

QY 348 PGYGNDSFNWMSGNYSSTRPSISNDIITSFYGNKSSEPVQNLFEENGKRYRAVANTN 407
DB 301 PGYGNDSFNWMSGNYSSTRPSISNDIITSFYGNKSSEPVQNLFEENGKRYRAVANTN 360

QY 408 LAVWPSAVYSGVTVERVSQYNDQDEASTQYDYSKRANVGAVSMSTIOQLPPTTDEPLEK 467
DB 361 LAVWPSAVYSGVTVERVSQYNDQDEASTQYDYSKRANVGAVSMSTIOQLPPTTDEPLEK 420

QY 468 GYSQOLNVKCFLMQSGHGTIPVLTWTHKSVDFNMIDSKKITQLPLVKAATKLOGSASV 527
DB 421 GYSQOLNVKCFLMQSGHGTIPVLTWTHKSVDFNMIDSKKITQLPLVKAATKLOGSASV 480

QY 528 AGPRTGDDIIQCTENGSAATITVTPDVYSQKRYARIRIHVASTQITFTTSLDCAPEQY 587
DB 481 AGPRTGDDIIQCTENGSAATITVTPDVYSQKRYARIRIHVASTQITFTTSLDCAPEQY 540

QY 588 YFDKTIKNGDILITNSFNLASFSTPFELSGNNLOIGVTLGASGRKYIDKIEFIPV 644
DB 541 YFDKTIKNGDILITNSFNLASFSTPFELSGNNLOIGVTLGASGRKYIDKIEFIPV 597

RESULT 13
US-08-705-438-2
Sequence 2, Application US/08705438
Patent No. 6015891
GENERAL INFORMATION:
APPLICANT: Adang, Michael J.
APPLICANT: Rochelleau, Thomas A.
APPLICANT: Merlo, Donald
APPLICANT: Murray, Elizabeth E.
TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallwanchik, Lloyd & Sallwanchik
STREET: 1000 Legion Place, Suite 1750
CITY: Orlando
STATE: Florida
COUNTRY: USA
ZIP: 32801

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,438
FILING DATE: 29-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
FILING DATE: 09-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-438-2

Query Match 92.5%; Score 3149; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.1e-255;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALSDSTTKDVYKIGISVVDLGVGFPFGALVSPYTNFLNTIMPSEDPMK 107
DB 1 MTADNNTALSDSTTKDVYKIGISVVDLGVGFPFGALVSPYTNFLNTIMPSEDPMK 60

QY 108 AFMEQVALMDOKIADYAKKALAELOGIANNEDVYSAISSWQKNPVSSRNHSGRR 167
DB 61 AFMEQVALMDOKIADYAKKALAELOGIANNEDVYSAISSWQKNPVSSRNHSGRR 120

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QY 168 ELFSQASHFRNSMPSAIGYEVLFITTYAQAANTHLLKDAQIYGEEMGEKEDIAE 227
| | | | |
DB 121 ELFSQASHFRNSMPSAIGYEVLFITTYAQAANTHLLKDAQIYGEEMGEKEDIAE 180
| | | | |
QY 228 FYKQOLKTOEYTHCHCKMYNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPELYD 287
| | | | |
DB 181 FYKQOLKTOEYTHCHCKMYNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPELYD 240
| | | | |
QY 288 VRLYPRKVEKTELTRDVLTDPIVGNVNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQ 347
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DB 241 VRLYPRKVEKTELTRDVLTDPIVGNVNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQ 300
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QY 348 PGYYGNSFNYSGNYSVTRPSIGSNDITSPFYGNKSSPVOVNLBNKGEKRYRAVANTN 407
| | | | |
DB 301 PGYYGNSFNYSGNYSVTRPSIGSNDITSPFYGNKSSPVOVNLBNKGEKRYRAVANTN 360
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QY 408 LAVWPSAVYSGVTVKEFSQYNDQDEASTQYDSKRNNGAVSMDSIDQLPPEITDEPLEK 467
| | | | |
DB 361 LAVWPSAVYSGVTVKEFSQYNDQDEASTQYDSKRNNGAVSMDSIDQLPPEITDEPLEK 420
| | | | |
QY 468 GYSHQOLNYVWCFLMQSGRGTIPVLTWTHKSVDFNMIDSKKITQLPLVYAKYKQSGASYV 527
| | | | |
DB 421 GYSHQOLNYVWCFLMQSGRGTIPVLTWTHKSVDFNMIDSKKITQLPLVYAKYKQSGASYV 480
| | | | |
QY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQKYYRARIHASTQSOTFTFLSLDGAPFNQY 587
| | | | |
DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQKYYRARIHASTQSOTFTFLSLDGAPFNQY 540
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QY 588 YFDKTIKNGDITLYNSFNLSFSTPELSGNNLQIGVTLGSLAGDKYIYDKIEFTIPV 644
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DB 541 YFDKTIKNGDITLYNSFNLSFSTPELSGNNLQIGVTLGSLAGDKYIYDKIEFTIPV 597
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```

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RESULT 14
US-08-704-966-4
; Sequence 4, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MFS 8-88AFD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-966-4

Query Match      92.3%; Score 3144; DB 3; Length 610;
Best Local Similarity 99.8%; Pred. No. 5.8e-255;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 48 MTADNTEALDSSTTKDVIQKGISVYGDLLGVGFPGGALVSTYTNFLNTIMPSEDPWK 107
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QY 108 AFMEQVEALMDQIADYAKNKALAELOGLQNNVEDYVSALSSWQKNVSSRNPHSQRIR 167
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DB 61 AFMEQVEALMDQIADYAKNKALAELOGLQNNVEDYVSALSSWQKNVSSRNPHSQRIR 120
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QY 168 ELFSQASHFRNSMPSAIGYEVLFITTYAQAANTHLLKDAQIYGEEMGEKEDIAE 227
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DB 121 ELFSQASHFRNSMPSAIGYEVLFITTYAQAANTHLLKDAQIYGEEMGEKEDIAE 180
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QY 228 FYKQOLKTOEYTHCHCKMYNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPELYD 287
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DB 181 FYKQOLKTOEYTHCHCKMYNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPELYD 240
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QY 288 VRLYPRKVEKTELTRDVLTDPIVGNVNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQ 347
| | | | |
DB 241 VRLYPRKVEKTELTRDVLTDPIVGNVNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQ 300
| | | | |
QY 348 PGYYGNSFNYSGNYSVTRPSIGSNDITSPFYGNKSSPVOVNLBNKGEKRYRAVANTN 407
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DB 301 PGYYGNSFNYSGNYSVTRPSIGSNDITSPFYGNKSSPVOVNLBNKGEKRYRAVANTN 360
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QY 408 LAVWPSAVYSGVTVKEFSQYNDQDEASTQYDSKRNNGAVSMDSIDQLPPEITDEPLEK 467
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DB 361 LAVWPSAVYSGVTVKEFSQYNDQDEASTQYDSKRNNGAVSMDSIDQLPPEITDEPLEK 420
| | | | |
QY 468 GYSHQOLNYVWCFLMQSGRGTIPVLTWTHKSVDFNMIDSKKITQLPLVYAKYKQSGASYV 527
| | | | |
DB 421 GYSHQOLNYVWCFLMQSGRGTIPVLTWTHKSVDFNMIDSKKITQLPLVYAKYKQSGASYV 480
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QY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQKYYRARIHASTQSOTFTFLSLDGAPFNQY 587
| | | | |
DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQKYYRARIHASTQSOTFTFLSLDGAPFNQY 540
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QY 588 YFDKTIKNGDITLYNSFNLSFSTPELSGNNLQIGVTLGSLAGDKYIYDKIEFTIPV 644
| | | | |
DB 541 YFDKTIKNGDITLYNSFNLSFSTPELSGNNLQIGVTLGSLAGDKYIYDKIEFTIPV 597
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RESULT 15
US-08-705-438-4
; Sequence 4, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/705,438
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-705-438-4
 Query Match 92.3%; Score 3144; DB 3; Length 610;
 Best Local Similarity 99.8%; Pred. No. 5,8e-255;
 Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 LAVMPSAVYSGVTKEFSQYNDQDEASTQTYDSKRNVAWSIDQLPPTTDEPLEK 420
 QY 468 GYSHOLNTVMCFIAMGSRGTIPVLTWTHKSYDFENMIDSKKITOLPLVKAYKLGASVY 527
 Db 421 GYSHOLNTVMCFIAMGSRGTIPVLTWTHKSYDFENMIDSKKITOLPLVKAYKLGASVY 480
 QY 528 AGPRTGGDIIOCTENGSAATLYVTPDVYSQKYRARIHYASTSOITFTLSLDGAPFNQY 587
 Db 481 AGPRTGGDIIOCTENGSAATLYVTPDVYSQKYRARIHYASTSOITFTLSLDGAPFNQY 540
 QY 588 YFDKTIINKGDILTYSFNLASFSTPELGGNNLQIGVTGLSAGDKVYTDKIEFIPVN 644
 Db 541 YFDKTIINKGDILTYSFNLASFSTPELGGNNLQIGVTGLSAGDKVYTDKIEFIPVN 597

Search completed: January 10, 2003, 11:08:25
 Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:06:34 ; Search time 11 Seconds

(without alignments)
1135.844 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406
Sequence: 1 MNPNNSEHDITKTENNEV.....TGLSAGDKVYIDKIEFIVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1214.5	35.7	673	12	US-10-032-717-18
4	1214.5	35.7	1210	12	US-10-032-717-4
5	1202.5	35.3	673	12	US-10-032-717-12
6	1195.5	35.1	667	12	US-10-032-717-22
7	1194.5	35.1	669	12	US-10-032-717-6
8	1194.5	35.1	669	12	US-10-032-717-10
9	1194.5	35.1	669	12	US-10-032-717-16
10	1194.5	35.1	669	12	US-10-032-717-40
11	1194.5	35.1	1206	12	US-10-032-717-2
12	1192	35.0	670	12	US-10-032-717-44
13	1189	34.9	670	12	US-10-032-717-24
14	1103.5	32.4	620	12	US-10-032-717-30
15	1096.5	32.2	620	12	US-10-032-717-32
16	1095.5	32.2	616	12	US-10-032-717-20
17	1095.5	32.2	620	12	US-10-032-717-42
18	1093	32.1	617	12	US-10-032-717-46
19	1090	32.0	617	12	US-10-032-717-34

20	1063.5	31.2	643	10	US-09-826-660-25	Sequence 25, Appl
21	1063.5	31.2	1166	10	US-09-826-660-23	Sequence 23, Appl
22	1044.5	30.7	655	10	US-09-826-660-27	Sequence 27, Appl
23	1012.5	29.7	1163	10	US-09-756-526A-2	Sequence 2, Appl1
24	980	28.8	1155	10	US-09-756-643-2	Sequence 2, Appl1
25	973	28.6	1177	10	US-09-873-873-26	Sequence 26, Appl
26	971	28.5	1177	10	US-09-873-873-28	Sequence 28, Appl
27	971	28.5	1177	10	US-09-873-873-34	Sequence 34, Appl
28	970	28.5	1177	10	US-09-873-873-10	Sequence 10, Appl
29	970	28.5	1177	10	US-09-873-873-12	Sequence 12, Appl
30	970	28.5	1177	10	US-09-873-873-14	Sequence 14, Appl
31	944.5	27.7	1163	10	US-09-826-660-21	Sequence 21, Appl
32	885	26.0	1193	10	US-09-873-873-30	Sequence 30, Appl
33	883.5	25.9	605	10	US-09-826-660-4	Sequence 4, Appl1
34	883.5	25.9	1148	10	US-09-826-660-2	Sequence 2, Appl1
35	883.5	25.9	1176	10	US-09-826-660-6	Sequence 6, Appl1
36	873.5	25.6	1316	9	US-10-120-544A-4	Sequence 4, Appl1
37	847	24.9	1332	9	US-10-120-544A-18	Sequence 18, Appl
38	845.5	24.8	1156	10	US-09-826-660-15	Sequence 15, Appl
39	845.5	24.8	1178	10	US-09-851-194-2	Sequence 2, Appl1
40	805	23.6	1386	9	US-10-120-544A-6	Sequence 6, Appl1
41	797.5	23.4	1344	9	US-10-120-544A-20	Sequence 20, Appl1
42	627	18.4	1109	10	US-09-756-526A-4	Sequence 4, Appl1
43	538.5	15.8	333	10	US-09-851-194-4	Sequence 4, Appl1
44	399	11.7	265	9	US-10-120-544A-8	Sequence 8, Appl1
45	391	11.5	153	9	US-10-120-544A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-943-692-2
; Sequence 2, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOET:195-1
; CURRENT APPLICATION NUMBER: US/09/943,692
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 2
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric toxin
US-09-943-692-2

Query Match 100.0%; Score 3406; DB 10; Length 644;
Best local Similarity 100.0%; Pred. No. 3e-258;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNSEHDITKTENNEVPTNHVOYPLAEPNPFLDNLNKEFLRMTADNNTEALDSS 60
DB 1 MNPNNSEHDITKTENNEVPTNHVOYPLAEPNPFLDNLNKEFLRMTADNNTEALDSS 60
QY 61 TTRDVIOKGISVVDLLGVGPFEGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
DB 61 TTRDVIOKGISVVDLLGVGPFEGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
QY 121 IADYAKKALAELOGLONNEDVYSALSWOKNPVSSRPHSGRTRELFSQAESHFRMS 180
DB 121 IADYAKKALAELOGLONNEDVYSALSWOKNPVSSRPHSGRTRELFSQAESHFRMS 180

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QY 181 MPEFAISGVEVLETTYAQAANTHFLKDAQIYGEEMGEYKEDIAEFYKROKLTQOEXT 240
DB 181 MPEFAISGVEVLETTYAQAANTHFLKDAQIYGEEMGEYKEDIAEFYKROKLTQOEXT 240
QY 241 DHCVKMYNNGDLKRGSSYESWVNFNRREMTLVLDLALFPLDVLVLYPREVTELT 300
DB 241 DHCVKMYNNGDLKRGSSYESWVNFNRREMTLVLDLALFPLDVLVLYPREVTELT 300
QY 301 RDVLTPIVGNVNLKRGYGTFSNIENYIRKPHLDYLRHIOFHTRPQPYGNDSPNYS 360
DB 301 RDVLTPIVGNVNLKRGYGTFSNIENYIRKPHLDYLRHIOFHTRPQPYGNDSPNYS 360
QY 361 GNVYSTRPSGNDITTSPEYGNKSEPVQNLFEENGKYYRAVANTNLAVMSAVYSGVT 420
DB 361 GNVYSTRPSGNDITTSPEYGNKSEPVQNLFEENGKYYRAVANTNLAVMSAVYSGVT 420
QY 421 KVEFSQYNDQTDASQYQYDSKRNKAVMSDSDOLPPTDEPLEKGSQHLNVMCL 480
DB 421 KVEFSQYNDQTDASQYQYDSKRNKAVMSDSDOLPPTDEPLEKGSQHLNVMCL 480
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DB 481 MGSQRTIVLWTWHSYDFPNMIDSKITQPLVKAYKLGASVAVGPRFTGGDIQC 540
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DB 541 TENGSAATITVTPDYSQYRARIHYASTQITTLSDGAPFQYQYFDKTIKNGDTLT 600
QY 601 YNSFNLSFSTPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLSFSTPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644

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RESULT 2

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US-10-032-717-8
; Sequence 8, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8

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Query Match 35.7%; Score 1214.5; DB 12; Length 667;
Best Local Similarity 39.0%; Pred. No. 5.3e-87;
Matches 268; Conservative 134; Mismatches 222; Indels 63; Gaps 20;
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DB 1 MSPNNQNEVEIITDPTSTSVSNDNRKYPFANPTNALQNDYDKYLMKSGNSEVPSP 60
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DB 61 EVLVSQDAKAAKAIIDIVGKLISGLGVPGPIVSLYQDLIDILPSQSKSOWETPEHPOVE 120
QY 115 ALMDQKADAKKAALELQGLONNVEDYVSAISSWQKNPVSSRNPHSOGRIEELPSQAE 174
DB 115 ALMDQKADAKKAALELQGLONNVEDYVSAISSWQKNPVSSRNPHSOGRIEELPSQAE 174

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DB 121 ELINQKIAEYANRANKLSELEGANNYOYLALAEKKNPNSGR---ALRDVNRNFEILD 177
QY 175 SHFRSMPSFAISGVEVLETTYAQAANTHFLKDAQIYGEEMGEYKEDIAEFYKROK 234
DB 175 SHFRSMPSFAISGVEVLETTYAQAANTHFLKDAQIYGEEMGEYKEDIAEFYKROK 234
QY 235 LTOEYTDHCVKMYNNGDLKRGSSYESWVNFNRREMTLVLDLALFPLDVLVLYPREVTELT 294
DB 235 LTOEYTDHCVKMYNNGDLKRGSSYESWVNFNRREMTLVLDLALFPLDVLVLYPREVTELT 294
QY 295 VKTELTRDVLTPDPIVGNVNLKRGYGTFSNIENYIRKPHLDYLRHIOFHTRPQPYGNDSPNYS 360
DB 295 VKTELTRDVLTPDPIVGNVNLKRGYGTFSNIENYIRKPHLDYLRHIOFHTRPQPYGNDSPNYS 360
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DB 361 GNVYSTRPSGNDITTSPEYGNKSEPVQNLFEENGKYYRAVANTNLAVMSAVYSGVT 420
QY 421 KVEFSQYNDQTDASQYQYDSKRNKAVMSDSDOLPPTDEPLEKGSQHLNVMCL 480
DB 421 KVEFSQYNDQTDASQYQYDSKRNKAVMSDSDOLPPTDEPLEKGSQHLNVMCL 480
QY 481 MGSQRTIVLWTWHSYDFPNMIDSKITQPLVKAYKLGASVAVGPRFTGGDIQC 540
DB 481 MGSQRTIVLWTWHSYDFPNMIDSKITQPLVKAYKLGASVAVGPRFTGGDIQC 540
QY 541 TENGSAATITVTPDYSQYRARIHYASTQITTLSDGAPFQYQYFDKTIKNGDTLT 600
DB 541 TENGSAATITVTPDYSQYRARIHYASTQITTLSDGAPFQYQYFDKTIKNGDTLT 600
QY 601 YNSFNLSFSTPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644
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RESULT 3

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US-10-032-717-18
; Sequence 18, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-18

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Query Match 35.7%; Score 1214.5; DB 12; Length 673;
Best Local Similarity 39.0%; Pred. No. 5.4e-87;
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TYPE: PRF
ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-12

Query Match 35.3%; Score 1202.5; DB 12; Length 673;
Best Local Similarity 39.1%; Pred. No. 4.7e-86;
Matches 268; Conservative 132; Mismatches 226; Indels 59; Gaps 21;

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QY 1 MNPNNSEHDITKTENNENPTNNHVOYPLAETPNPTLEDLNTKEFLMTADNTEALDSS 60
DB 1 MSPNNONEYEIIDATPSTSVSNDNRYPFANPEPNALQNMDDKDLKMSAGNASEYPCSP 60
QY 61 ----TTKDVIGKISVYVGLLVGVPFGALVSEYTNFLNTMPS--EDPKAFMEQVE 114
DB 61 EVLVSGODAKAALIDIVKLGSLGVFPVGPVSVLYTLQDILIMPSEKQWEIEMEVE 120
QY 115 ALMDOKIADYAKNKAALAELOGLQNNVEDVYALSQKPNVSSRNPHSGR-IRELFSGA 173
DB 121 ELINOKIAEYAKNKAALAELOGLQNNVQYLTLEEMENPNKSNRSLALRDVRRNFEL 180
QY 174 ESHFRNMPSPALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 233
DB 181 DSELYQMPSPALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 240
QY 234 KLTOEYTHDCVKNYNGLDKLGSSYSEWVNFNRRREMTLVLDLALFPLDYVLYPK 293
DB 241 KLTAEYSDHCVKMYETGLAKLKTSAKQWVDNFRREMTLAVLDVALFPYDTRTYPM 300
QY 294 EVKTELTDVLTDPITGVNVLNGYGT-----TFSNIE-NYIRKPHLDYLRHIOFHR- 345
DB 301 ETKAQLTREVYTDPL-GAVNVSSISGWYDKAPSEGVIESVIRPHVFDYITGLTYTQS 359
QY 346 --FQPGYGNDSFNWYSGNVY--TRPSIGSNDIITSPRYG-KKSEPVONLENGEKYR 401
DB 360 RSISSARY-----IRHAGHOISTHRYVSRGSN---LOOMYGTNOMLHSTSTEDFTNYDIYK 412
QY 402 AVANTNL---AVMP--SAVYSGVTKVEFSQYNDQDEASTOTYDS-KRNVGAVMSDSIQ 455
DB 413 TLSKQAVLDLIVPGTYITFGMPVEVEFMVNOINRTKLYNPVSKDIIASTDSELE 472
QY 456 LPPEITDEPLEKYSVOLNYMCFMLOG-SRGTIPVLTWTHKSVDFNMIDSKKITOLPL 514
DB 473 LPPEITDQPNYESYSHRLCHITISIPATGNTGLVPFVSWTHRSADLNTIYSDKITOIPA 532
QY 515 VKAYKLGASVAVAGPRFTGDIIOCTEN-GSAATITVTP--DVSYSOKYARAHVAST 570
DB 533 VKCWDNLPEVPVYKPGHGTGDLQYNRSTGSVGLFLARGLALEKAKYRVRRLRYATD 592
QY 571 SQTFTLSLDGAPFNQYEDKTIKNGDILTYNSFNLSFSTPEELS-----GNN 619
DB 593 ADI--VLHVND--QIOMPRTMNGEDLTSKTFKVADAITTLNLATDSSLAKHNLGED 647
QY 620 LQIGVGLSAGDKYIDKIEFIPV 644
DB 648 PNSTLSGI-----VYDRIEFIPVD 667

```

RESULT 6
US-10-032-717-22
Sequence 22, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 673
TYPE: PRF
ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-22

Query Match 35.1%; Score 1195.5; DB 12; Length 673;
Best Local Similarity 38.8%; Pred. No. 1.7e-85;
Matches 266; Conservative 133; Mismatches 227; Indels 59; Gaps 21;

```

QY 1 MNPNNSEHDITKTENNENPTNNHVOYPLAETPNPTLEDLNTKEFLMTADNTEALDSS 60
DB 1 MSPNNONEYEIIDATPSTSVSNDNRYPFANPEPNALQNMDDKDLKMSAGNASEYPCSP 60
QY 61 ----TTKDVIGKISVYVGLLVGVPFGALVSEYTNFLNTMPS--EDPKAFMEQVE 114
DB 61 EVLVSGODAKAALIDIVKLGSLGVFPVGPVSVLYTLQDILIMPSEKQWEIEMEVE 120
QY 115 ALMDOKIADYAKNKAALAELOGLQNNVEDVYALSQKPNVSSRNPHSGR-IRELFSGA 173
DB 121 ELINOKIAEYAKNKAALAELOGLQNNVQYLTLEEMENPNKSNRSLALRDVRRNFEL 180
QY 174 ESHFRNMPSPALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 233
DB 181 DSELYQMPSPALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 240
QY 234 KLTOEYTHDCVKNYNGLDKLGSSYSEWVNFNRRREMTLVLDLALFPLDYVLYPK 293
DB 241 KLTAEYSDHCVKMYETGLAKLKTSAKQWVDNFRREMTLAVLDVALFPYDTRTYPM 300
QY 294 EVKTELTDVLTDPITGVNVLNGYGT-----TFSNIE-NYIRKPHLDYLRHIOFHR- 345
DB 301 ETKAQLTREVYTDPL-GAVNVSSISGWYDKAPSEGVIESVIRPHVFDYITGLTYTQS 359
QY 346 --FQPGYGNDSFNWYSGNVY--TRPSIGSNDIITSPRYG-KKSEPVONLENGEKYR 401
DB 360 RSISSARY-----IRHAGHOISTHRYVSRGSN---LOOMYGTNOMLHSTSTEDFTNYDIYK 412
QY 402 AVANTNL---AVMP--SAVYSGVTKVEFSQYNDQDEASTOTYDS-KRNVGAVMSDSIQ 455
DB 413 TLSKQAVLDLIVPGTYITFGMPVEVEFMVNOINRTKLYNPVSKDIIASTDSELE 472
QY 456 LPPEITDEPLEKYSVOLNYMCFMLOG-SRGTIPVLTWTHKSVDFNMIDSKKITOLPL 514
DB 473 LPPEITDQPNYESYSHRLCHITISIPATGNTGLVPFVSWTHRSADLNTIYSDKITOIPA 532
QY 515 VKAYKLGASVAVAGPRFTGDIIOCTEN-GSAATITVTP--DVSYSOKYARAHVAST 570
DB 533 VKCWDNLPEVPVYKPGHGTGDLQYNRSTGSVGLFLARGLALEKAKYRVRRLRYATD 592
QY 571 SQTFTLSLDGAPFNQYEDKTIKNGDILTYNSFNLSFSTPEELS-----GNN 619
DB 593 ADI--VLHVND--QIOMPRTMNGEDLTSKTFKVADAITTLNLATDSSLAKHNLGED 647
QY 620 LQIGVGLSAGDKYIDKIEFIPV 644
DB 648 PNSTLSGI-----VYDRIEFIPVD 667

```

RESULT 7
US-10-032-717-6
Sequence 6, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn

```

: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Pesticide Encoding No. US20020151709A1 Proteins With
: TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032.717
: CURRENT FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: PRIOR FILING DATE: 2000-10-24
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 667
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (truncated)
: US-10-032-717-6

```

Db 645 NSTLSGI-----YVDRIEFIPVD 663

RESULT 9

US-10-032-717-16

Sequence 16, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Slims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 669
TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (truncated)
US-10-032-717-16

Query Match 35.1%; Score 1194.5; DB 12; Length 669;
Best Local Similarity 38.9%; Pred. No. 2e-65;
Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

QY 1 MNPNNSEHDITKTENNEVPNHYOPLAETPNPLEDINKEFLRMTADNTEALDSS 60
DB 1 MSPNNQNEYIIDATPSTSVSNDNRYPANEPNALQNMOKYKOLKMSAGASBPSP 60
QY 61 -----TTKDVOKGIVSGDGLGVGPPFGALVSFTYNTFLTWPS--EDPKAMEQVE 114
DB 61 EYLVSGDAKAAIDIVGLKLSGLGVPVGPVSLYTLQILIMPSEKSGOMEIFMEQVE 120
QY 115 ALMDQKIDYAKKALAELOGIANNVEDYVSALSMOKNPVSSRNPHSGRIREFSQA 174
DB 121 ELINOKIAEYARRKALSELEGNNYQVLYLALKEEENPNSGR--ALRDVNRFEILD 177
QY 175 SHFRSMSPFASISGEVLEFLTYAQAANTHLELKDAQIYGEWYKEDIAEFYKROL 234
DB 178 SLFQYMPSPFRTNFEVPLTYAAMAHLKLDASIFGEWGWSTTTNNYIDRQM 237
QY 235 LTOEYTHDCVKNYNGDLKLRSSYESVWNNRRRENTLYLALFLPLDYRLPK 294
DB 238 LTAETSDHCVMYETGLKLGTSKQWVDNFRRENTLAVLVAFNPDRTTYPM 297
QY 295 VKTELTROYLDPIYGVNNGKGYT-----TFSNIE-NYTRKPHLDYLRIOFHR-- 345
DB 298 TKAOLTRREVYDPL-GAVNVSSIGSWDKAPFVIESVIRPHVVDYITGLVYVQSR 356
QY 346 -FQGYGNDSEFNWWSGYVS-TRPSIGSNDIITSPTFG-KKSEPVQONLEFNGEKYRA 402
DB 357 SISSARY-----IRHWAGQIISYHVSRSN--LQOMGTQONLHSTFDFTYDIYKT 409
QY 403 VANTNL--AWP--SAVYSGTVKEFSQYNDQDEASTQYDS-KNNGVAVSDSIDOL 456
DB 410 LSKRAVLDDIYVPGTYIFFGMPVEFEFPMVQNLNTRKTLKYNVSKDIIASTDSLEL 469
QY 457 PPEPTDEPLEKGYSHQNLVYVCLMUG-SRGTLPVLVLTWTHKSVDFNMIDSKRTIOLPLV 515
DB 470 PPEPTSDPNTESYHRLCHITSIPATGNTGLVGVESWTHRSADLNTITISDKITQIPAY 529
QY 516 KAYVLOGSASVAVGPRRTGGDIIOCTEN-GSAATITVP--DVYSQKRYARIHVA 571
DB 530 KCMONLFPVAVVGGPHTGDDLOYNRSTGSGVGLFLARYGLALEKAGKYRVLRYATDA 589

QY 572 QITFTLSLDGAPFPNOYEDKTIKNGDTLTYNSENLASESTPEELS-----GNUL 620
DB 590 DI--VLHVND-----OIQMPKTWNGEDILTSKTFKVAADATITLNLATDSLAKHNLGDEP 644
QY 621 QIGVGLSAGDKVYIDKIEFIPV 644
DB 645 NSTLSGI-----YVDRIEFIPVD 663

RESULT 10

US-10-032-717-40

Sequence 40, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Slims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 673
TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (mutated)
US-10-032-717-40

Query Match 35.1%; Score 1194.5; DB 12; Length 673;
Best Local Similarity 38.8%; Pred. No. 2e-65;
Matches 266; Conservative 133; Mismatches 227; Indels 59; Gaps 21;

QY 1 MNPNNSEHDITKTENNEVPNHYOPLAETPNPLEDINKEFLRMTADNTEALDSS 60
DB 1 MSPNNQNEYIIDATPSTSVSNDNRYPANEPNALQNMOKYKOLKMSAGASBPSP 60
QY 61 -----TTKDVOKGIVSGDGLGVGPPFGALVSFTYNTFLTWPS--EDPKAMEQVE 114
DB 61 EYLVSGDAKAAIDIVGLKLSGLGVPVGPVSLYTLQILIMPSEKSGOMEIFMEQVE 120
QY 115 ALMDQKIDYAKKALAELOGIANNVEDYVSALSMOKNPVSSRNPHSGRIREFSQA 173
DB 121 ELINOKIAEYARRKALSELEGNNYQVLYLALKEEENPNSGR--ALRDVNRFEILD 180
QY 174 SHFRSMSPFASISGEVLEFLTYAQAANTHLELKDAQIYGEWYKEDIAEFYKROL 233
DB 181 DLFQYMPSPFRTNFEVPLTYAAMAHLKLDASIFGEWGWSTTTNNYIDRQM 240
QY 234 KLTQYTHDCVKNYNGDLKLRSSYESVWNNRRRENTLYLALFLPLDYRLPK 293
DB 241 LTAETSDHCVMYETGLKLGTSKQWVDNFRRENTLAVLVAFNPDRTTYPM 300
QY 294 EVTELTROYLDPIYGVNNGKGYT-----TFSNIE-NYTRKPHLDYLRIOFHR-- 345
DB 301 ETKAOLTRREVYDPL-GAVNVSSIGSWDKAPFVIESVIRPHVVDYITGLVYVQSR 359
QY 346 -FQGYGNDSEFNWWSGYVS-TRPSIGSNDIITSPTFG-KKSEPVQONLEFNGEKYRA 401
DB 360 RSISSARY-----IRHWAGQIISYHVSRSN--LQOMGTQONLHSTFDFTYDIYKT 412
QY 402 VANTNL--AWP--SAVYSGTVKEFSQYNDQDEASTQYDS-KNNGVAVSDSIDOL 455
DB 413 TSKRAVLDDIYVPGTYIFFGMPVEFEFPMVQNLNTRKTLKYNVSKDIIASTDSLE 472
QY 456 LPEPTDEPLEKGYSHQNLVYVCLMUG-SRGTLPVLVLTWTHKSVDFNMIDSKRTIOLPL 514

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Db 473 LPEPESDQNVYESYSHRLCHTISIPATGNTGLVPEFSWTHRSADLNNTIYSDKITQIIPA 532
Oy 515 VKAYKIQSASVAVGPRFGCDIIQCTEN-GSAATITVP---DVSYSQYARARIHAYST 570
Db 533 KCMWMLPEVPYVKGHGGHGLDLOYNRSTGVLFLARGLALEKAKYVRLRYATDA 592
Oy 571 SOTFTLSLDGAFENQYFDKTIKNGDITLYNSFNLSASTPEELS-----GNN 619
Db 593 ADI--VLHVND---OIQMPKTMNPGEDLTSKTFKVAADITTLNLTATDSLAKHNLGSD 647
Oy 620 LOIGVTGLSAGDKVYIDKIEFIPVN 644
Db 648 PNSTLSGI-----VYVDRIEFIPVD 667

RESULT 11
US-10-032-717-2
; Sequence 2, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 35.1%; Score 1194.5; DB 12; Length 1206;
Best Local Similarity 38.9%; Pred. No. 4.7e-85;
Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

Oy 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPLEDLNKEFLMTADNTEALDSS 60
Db 1 MSPNNQNEYELIDATPSTSVSNDNRYPFANEPTNLQNDYKDYDKMSAGNASEYFGSP 60
Oy 61 ----TTKDVIOKGISVVGDLGVGPFPGALVSFTNPLNTIWP--EDPWKAEMEYVE 114
Db 61 EVLVSGDAAKAALIDYIGKLLSGIGVPGPIVSLYQLDILMPGSKSQWEIFMEQVE 120
Oy 115 ALMDOKIADYAKNALAELOGLONNVEDYVLSWSQKNPVSNSQGRIRLEFSQAE 174
Db 121 ELINOKIAEYARNAKALSELGLGNNGYOLYLTALEBEMENPNSR--ALRDVNRREIFLD 177
Oy 175 SHFRNSMSPFASISGEVLEFLTYAQAANTHLFLKDAQIYEGEWYKEDIAEYFROK 234
Db 178 SLFTQYMSERFVTEFEVFLTYMAANLHLKDSIFEEGWSSTTINNYDRMK 237
Oy 235 VKTELTRDVLDPITGVANNLKGYGT-----TFSNIE-NYIRKPHLFDYLRIQFHTR-- 345
Db 238 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 297
Oy 235 LTOEYTDHCYKWNVVGDLKRGSSYESVNFNRKREMTLVLDLALFPLYDVRLPYKE 294
Db 238 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 297
Oy 235 VKTELTRDVLDPITGVANNLKGYGT-----TFSNIE-NYIRKPHLFDYLRIQFHTR-- 345
Db 238 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 297
Oy 235 LTOEYTDHCYKWNVVGDLKRGSSYESVNFNRKREMTLVLDLALFPLYDVRLPYKE 294
Db 238 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 297
Oy 346 -FQPGYGCNDSPNYSNGVVS--TRPSIGSNDITSPFG-KNSSEPVONLENGEKYVRA 402
Db 357 SSISSARY-----IRHAGHDIHYHRSRGN--LQOMGTGNQNLHSTSPFDNTDIYKT 409

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Oy 403 VANTNL---AWP--SAVYSCVTKVESQYDQDEASTQTYDS-KRNGAVSNDSDIOL 456
Db 410 LSKDAVLVDIYVGYTYIFGMPMEVEEFMNQNLNTRRTLEKYNVSDIADISTDSELEL 469
Oy 457 PPEPDEPLEKGYSHQNLVWYCMFMOG--SRGTIPVMTHTKSVDFPNIDSKITOLPLV 515
Db 470 PPEPESDQNVYESYSHRLCHTISIPATGNTGLVPEFSWTHRSADLNNTIYSDKITQIIPA 529
Oy 516 KAYKIQSASVAVGPRFGCDIIQCTEN-GSAATITVP---DVSYSQYARARIHAYST 571
Db 530 KCMWMLPEVPYVKGHGGHGLDLOYNRSTGVLFLARGLALEKAKYVRLRYATDA 589
Oy 572 QITFTLSLDGAFENQYFDKTIKNGDITLYNSFNLSASTPEELS-----GNNL 620
Db 590 DI--VLHVND---OIQMPKTMNPGEDLTSKTFKVAADITTLNLTATDSLAKHNLGSD 644
Oy 621 QIGVTGLSAGDKVYIDKIEFIPVN 644
Db 645 NSTLSGI-----VYVDRIEFIPVD 663

RESULT 12
US-10-032-717-44
; Sequence 44, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 670
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-44

Query Match 35.0%; Score 1192; DB 12; Length 670;
Best Local Similarity 38.7%; Pred. No. 3.1e-85;
Matches 265; Conservative 134; Mismatches 225; Indels 60; Gaps 21;

Oy 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPLEDLNKEFLMTADNTEALDSS 60
Db 1 MSPNNQNEYELIDATPSTSVSNDNRYPFANEPTNLQNDYKDYDKMSAGNASEYFGSP 60
Oy 61 ----TTKDVIOKGISVVGDLGVGPFPGALVSFTNPLNTIWP--EDPWKAEMEYVE 114
Db 61 EVLVSGDAAKAALIDYIGKLLSGIGVPGPIVSLYQLDILMPGSKSQWEIFMEQVE 120
Oy 115 ALMDOKIADYAKNALAELOGLONNVEDYVLSWSQKNPVSNSQGRIRLEFSQAE 174
Db 121 ELINOKIAEYARNAKALSELGLGNNGYOLYLTALEBEMENL--RMSRALDVNRREIFLD 178
Oy 175 SHFRNSMSPFASISGEVLEFLTYAQAANTHLFLKDAQIYEGEWYKEDIAEYFROK 234
Db 178 SLFTQYMSERFVTEFEVFLTYMAANLHLKDSIFEEGWSSTTINNYDRMK 238
Oy 235 VKTELTRDVLDPITGVANNLKGYGT-----TFSNIE-NYIRKPHLFDYLRIQFHTR-- 345
Db 238 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 298
Oy 235 LTOEYTDHCYKWNVVGDLKRGSSYESVNFNRKREMTLVLDLALFPLYDVRLPYKE 294
Db 239 LTAESYDHCYKWEYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPYVDRTYPM 298
Oy 295 VKTELTRDVLDPITGVANNLKGYGT-----TFSNIE-NYIRKPHLFDYLRIQFHTR-- 345

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Db 299 TKAOITREYTDPL-GAVNVSSIGSWYDKAPSEGVIESSEYIRPPHVEDYITGLTVYQSR 357
QY 346 -FOGYGNDSEFNWNGNYS--TRPSIGSNDITSPFYG--NKSEPEVONLEFNGEKYRA 402
Db 358 SISARV-----IRHWAGHOISYHRVRSN---LOOMGTNOLNHSSTPFDNYDITKT 410
QY 403 VANTNL---AVWP--SAVSGVTKVEFSQYNDQDEASTQYDS--KRNVAWSIDSIDL 456
Db 411 LSKDAVLDDIYVGYTYFEFGMEVEFPMVQNLNTRKTLKYPVKDIIASRDELEL 470
QY 457 PPTDEPLEKGYSHOLNYMCFMLOG--SRGTIPVLTWTHKSVDFFNMIDSKRTTOLPLV 515
Db 471 PPTSDQPNYESYSHRCHITTSIPATGNTGLVPEFSTHRSADLNNTTYSDKITQIPAV 530
QY 516 KAYKLGASVAVGPRFTGDIIOCTEN--GSAATIVYTP--DVSYSOKYRARIHYASTS 571
Db 531 KCDNMLPEVYVVGPGHGTGDLQYNRSQSVGTFLARYGLALEKAGKRYRLRYATDA 590
QY 572 QITFTLSLDGAPFNOYFEDKTIKNGDLYNSFNILASFSTPELS-----GNL 620
Db 591 DI--VLHVND---QIOMPKTMNGEDLTSKTEKVAITTLNLATDSLALKHNLGEDP 645
QY 621 QIGVTGLSAGDKVYIDKIEFIPV 644
Db 646 NSTLSGI-----YVDRIEFIPVD 664

```

RESULT 13

```

US-10-032-717-24
: Sequence 24, Application US/10032717
: Patent No. US20020151709A1
: GENERAL INFORMATION:
: APPLICANT: Andre R. Abad
: APPLICANT: Nicholas B. Duck
: APPLICANT: Xiang Feng
: APPLICANT: Ronald D. Flanagan
: APPLICANT: Theodore W. Kahn
: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
: TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032,717
: PRIOR FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 670
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-24

```

```

Query Match 34.9%; Score 1189; DB 12; Length 670;
Best Local Similarity 38.6%; Pred. No. 5,3e-85;
Matches 264; Conservative 135; Mismatches 225; Indels 60; Gaps 21;

```

```

QY 1 MNPNRSHDITKTENNEVPNVOYPLAETPMTLEDLNYKEFLRMTADNTEALDSS 60
Db 1 MSPNNQNEYETIDATPSYVSNDNRYPFANEPTNALQNMIDYKDYLMKMSAGNASEPGSP 60
QY 61 -----TTKVIQKISVGDILGVGPGGALVSFTYNTLNTWPS--EDPWKAFMQVE 114
Db 61 EVLVSGDAAKAIDIVGKLSGIVPVGPIVSLYQLDILMPSEKQWELFMQVE 120
QY 115 ALMDOKIADYAKKALAELOGIQQNVEDYVSAISSMOKNPVSSRNPSQGRIRLFQDAE 174
Db 121 ELINOKIAEYARKKALAELEGLGNNYQLYLALAEWEEENP--KMSALADVNRREFIIL 178
QY 175 SHFNKSPFAISGYEVLFTTYQAANTHLFLKDAQIYGEWGYEKEDIAPFYKROK 234
Db 179 SLFOYMSFPAVTNFEVPLTVYMAANLHLHLKLDASIGFEGMGWSTTTINNYDROMK 238

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```

QY 235 LFOETDHCYKYNGLDKRGSSYESVNNRNRREMTLTVLIDALFPLDYRLYPE 294
Db 239 LTAEYSDHCYKYNGLDKRGSSYESVNNRNRREMTLTVLIDALFPLDYRLYPE 298
QY 295 VKTELRDYLTPPIYGVNNLRGCT-----TFESIE--NYIRKPLFYLRIQFHR-- 345
Db 299 TKAOITREYTDPL-GAVNVSSIGSWYDKAPSEGVIESSEYIRPPHVEDYITGLTVYQSR 357
QY 346 -FOGYGNDSEFNWNGNYS--TRPSIGSNDITSPFYG--NKSEPEVONLEFNGEKYRA 402
Db 358 SISARV-----IRHWAGHOISYHRVRSN---LOOMGTNOLNHSSTPFDNYDITKT 410
QY 403 VANTNL---AVWP--SAVSGVTKVEFSQYNDQDEASTQYDS--KRNVAWSIDSIDL 456
Db 411 LSKDAVLDDIYVGYTYFEFGMEVEFPMVQNLNTRKTLKYPVKDIIASRDELEL 470
QY 457 PPTDEPLEKGYSHOLNYMCFMLOG--SRGTIPVLTWTHKSVDFFNMIDSKRTTOLPLV 515
Db 471 PPTSDQPNYESYSHRCHITTSIPATGNTGLVPEFSTHRSADLNNTTYSDKITQIPAV 530
QY 516 KAYKLGASVAVGPRFTGDIIOCTEN--GSAATIVYTP--DVSYSOKYRARIHYASTS 571
Db 531 KCDNMLPEVYVVGPGHGTGDLQYNRSQSVGTFLARYGLALEKAGKRYRLRYATDA 590
QY 572 QITFTLSLDGAPFNOYFEDKTIKNGDLYNSFNILASFSTPELS-----GNL 620
Db 591 DI--VLHVND---QIOMPKTMNGEDLTSKTEKVAITTLNLATDSLALKHNLGEDP 645
QY 621 QIGVTGLSAGDKVYIDKIEFIPV 644
Db 646 NSTLSGI-----YVDRIEFIPVD 664

```

RESULT 14

```

US-10-032-717-30
: Sequence 30, Application US/10032717
: Patent No. US20020151709A1
: GENERAL INFORMATION:
: APPLICANT: Andre R. Abad
: APPLICANT: Nicholas B. Duck
: APPLICANT: Xiang Feng
: APPLICANT: Ronald D. Flanagan
: APPLICANT: Theodore W. Kahn
: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
: TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032,717
: PRIOR FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 620
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-30

```

```

Query Match 32.4%; Score 1103.5; DB 12; Length 620;
Best Local Similarity 39.5%; Pred. No. 2,3e-78;
Matches 252; Conservative 117; Mismatches 210; Indels 59; Gaps 21;

```

```

QY 48 MTADNTEALDSS-----TKDVIQKISVGDILGVGPGGALVSFTYNTLNTWPS- 102
Db 1 MSAAGNASEPGSEVLVSGDAAKAIDIVGKLSGIVPVGPIVSLYQLDILMPSPG 60
QY 103 -EDPWKAFMQVEALMDOKIADYAKKALAELOGIQQNVEDYVSAISSMOKNPVSSRNPS 161
Db 61 EKSQWELFMQVEALMDOKIADYAKKALAELEGLGNNYQLYLALAEWEEENPNSRGS 120
QY 162 SQCR-IRLFQSAESHFNKSPFAISGYEVLFTTYQAANTHLFLKDAQIYGEWGY 220

```

```

Db 121 RALDVNNRFEILDSLTQYMPSEFRVNFPEPLTYVAMANLHLKLSKASJFGEEMGW 180
QY 221 EKEDIAEFYKROLKTQYETHDCVKWYNVGLDKRGSSYESWVNFNRRREMTLVLDLI 280
Db 181 STTINNYYDRQMKLTAEVSDHCWKWYETGLAKTSAQWVDYNQFRREMTLVLDVY 240
QY 281 ALFPLVDVLYKREVKETELTRDVLDPYGVNNLKGCT-----TFSNIE-NYIRKPHL 333
Db 241 ALFPNDTFTYPMETKAQLTRVYTDPL-GAVNVSSIGSWYDKAPSGVIESVIRPPHV 299
QY 334 FDLHRIQFTR---FQPGYGNDSFNWGSNYS-TRPSIGSNDITTSFYG-NKSSP 388
Db 300 FDTITGLTYTQSRSSSAR-----IRHAGHOISYHRVSRGN---LQMTGTNQLHS 352
QY 389 VONLENGEKYRAVANNTNL---AWP--SAVYSGVTKVEFSQYNDQDEASTQYDS-K 442
Db 353 TSFDFNTNDIYKTLSDAVLDIYVPGYTYIFGMEVEFEFVNNQNNTRKTLKPNVS 412
QY 443 RNNGAVSMDSIDLPETDEPLEKGYSHQNLVYMCFLMG-SRGTIYLVLTWTKSVDFP 501
Db 413 KDIIASTRDELELPETSDQPNYESYSHRLCHITSIPATGNTGLVPSWTHRSADLN 472
QY 502 NMIDSKITQLPLVYAKKLGASVYAGPRFTGDIIOCTEN-GSAATYVTP---DVS 557
Db 473 NTIYSDKITQIPAVKCMNDLPFVYVKGPGHGTGDLQYNRSTGVSGLFLARYGLALEK 532
QY 558 SOKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDTLTYNSFNILASFSTPELS- 616
Db 533 AGKYRVLRYATDADI--VLHVND--QIQMPKTMNPGEDLTSKTFKVAADITTLNAT 587
QY 617 -----GNNLOIGVYGLSAGDKYITDKIEFPVN 644
Db 588 DSSLAKHNLGDEPNSTLSGI-----VYDRIEFIPVD 620

```

RESULT 15

```

US-10-032-717-32
: Sequence 32, Application US/10032717
: Patent No. US20020151709A1
: GENERAL INFORMATION:
: APPLICANT: Andre R. Abad
: APPLICANT: Nicholas B. Duck
: APPLICANT: Xiang Peng
: APPLICANT: Ronald D. Flannagan
: APPLICANT: Theodore W. Kahn
: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032,717
: PRIOR FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 32
: LENGTH: 620
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (mutated)
: US-10-032-717-32

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Query Match 32.2%; Score 1096.5; DB 12; Length 620;

Best Local Similarity 39.2%; Pred. No. 7.9e-78;

Matches 250; Conservative 118; Mismatches 211; Indels 59; Gaps 21;

```

QY 48 MPADNTEALDSS---TTKDYIOKGISVVDLGVGFPGGALVSFTYNPLNTMP- 102
Db 1 MSAGNASEYPGSPVYSGDAKKAIDIVGKLSGLGVFPVGPISYLTQIDLIIPSG 60
QY 103 -EDPKAFMEQVADMDOKTADYAKKALAELOGLONNVEDYVSALSSWQKNFVSSRNPH 161
Db 61 EKQWEIFMEQVDELINOKIAEYARNKALSELGLGNNOYLYLTALAEWEENPLKMSNGS 120

```

```

QY 162 SOGR-IRELISOAESHRFNSMPSFAISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGY 220
Db 121 RALDVNNRFEILDSLTQYMPSEFRVNFPEPLTYVAMANLHLKLSKASJFGEEMGW 180
QY 221 EKEDIAEFYKROLKTQYETHDCVKWYNVGLDKRGSSYESWVNFNRRREMTLVLDLI 280
Db 181 STTINNYYDRQMKLTAEVSDHCWKWYETGLAKTSAQWVDYNQFRREMTLVLDVY 240
QY 281 ALFPLVDVLYKREVKETELTRDVLDPYGVNNLKGCT-----TFSNIE-NYIRKPHL 333
Db 241 ALFPNDTFTYPMETKAQLTRVYTDPL-GAVNVSSIGSWYDKAPSGVIESVIRPPHV 299
QY 334 FDLHRIQFTR---FQPGYGNDSFNWGSNYS-TRPSIGSNDITTSFYG-NKSSP 388
Db 300 FDTITGLTYTQSRSSSAR-----IRHAGHOISYHRVSRGN---LQMTGTNQLHS 352
QY 389 VONLENGEKYRAVANNTNL---AWP--SAVYSGVTKVEFSQYNDQDEASTQYDS-K 442
Db 353 TSFDFNTNDIYKTLSDAVLDIYVPGYTYIFGMEVEFEFVNNQNNTRKTLKPNVS 412
QY 443 RNNGAVSMDSIDLPETDEPLEKGYSHQNLVYMCFLMG-SRGTIYLVLTWTKSVDFP 501
Db 413 KDIIASTRDELELPETSDQPNYESYSHRLCHITSIPATGNTGLVPSWTHRSADLN 472
QY 502 NMIDSKITQLPLVYAKKLGASVYAGPRFTGDIIOCTEN-GSAATYVTP---DVS 557
Db 473 NTIYSDKITQIPAVKCMNDLPFVYVKGPGHGTGDLQYNRSTGVSGLFLARYGLALEK 532
QY 558 SOKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDTLTYNSFNILASFSTPELS- 616
Db 533 AGKYRVLRYATDADI--VLHVND--QIQMPKTMNPGEDLTSKTFKVAADITTLNAT 587
QY 617 -----GNNLOIGVYGLSAGDKYITDKIEFPVN 644
Db 588 DSSLAKHNLGDEPNSTLSGI-----VYDRIEFIPVD 620

```

Search completed: January 10, 2003, 11:08:43

Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:04:59 ; Search time 21 Seconds

(without alignments)
2948.122 Million cell updates/sec

Title: US-09-943-692-2

Sequence: 1 MHPNNRSEHDITKTENNEV.....TGLSAGDKVYIDKIEIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3406	100.0	652	2 A27323	parasporal crystal
2	2564.5	75.3	649	1 JH0261	parasporal crystal
3	2341.5	68.7	652	2 I39811	parasporal crystal
4	2307.5	67.7	659	2 S10228	parasporal crystal
5	1178	34.6	719	2 I40590	crystal -
6	1156	33.9	719	2 I39815	insecticidal prote
7	1152.5	33.8	1138	2 A48944	parasporal crystal
8	1149	33.7	1157	1 S49247	parasporal crystal
9	1147	33.7	719	2 S25383	parasporal crystal
10	1147	33.7	719	2 I39814	insecticidal prote
11	1109	32.6	1228	2 S00873	parasporal crystal
12	1034.5	30.4	1160	2 I40569	parasporal crystal
13	988	29.0	1154	2 S39536	parasporal crystal
14	980	28.8	1155	2 A26513	parasporal crystal
15	980	28.8	1155	2 J00002	parasporal crystal
16	980	28.8	1156	2 A29125	parasporal crystal
17	971.5	28.5	1181	2 A41052	parasporal crystal
18	969	28.4	1155	2 I39838	parasporal crystal
19	967	28.4	1155	2 S02134	parasporal crystal
20	954.5	28.0	934	2 A22798	parasporal crystal
21	948.5	27.8	1176	2 J02041	parasporal crystal
22	944.5	27.7	655	2 J02140	protoxin - Bacillu
23	943.5	27.7	1176	2 J02219	parasporal crystal
24	938.5	27.6	1176	2 A22617	parasporal crystal
25	938.5	27.6	1176	2 S02215	parasporal crystal
26	929.5	27.3	1189	2 S00944	parasporal crystal
27	929.5	27.3	1176	2 A48970	parasporal crystal
28	912.5	26.8	823	2 S04181	parasporal crystal
29	911.5	26.8	1166	2 S32645	parasporal crystal

30	895.5	26.3	1156	2 A29838	parasporal crystal
31	883.5	25.9	1174	2 A42459	parasporal crystal
32	883	25.9	1171	2 A37829	parasporal crystal
33	883	25.9	1171	2 I40572	parasporal crystal
34	882	25.9	1174	2 S32649	parasporal crystal
35	852	25.0	1165	2 S11446	parasporal crystal
36	847	24.9	1177	2 A49785	parasporal crystal
37	845.5	24.8	1178	2 USB5X8	parasporal crystal
38	841	24.7	618	2 S11445	parasporal crystal
39	835.5	24.5	1160	2 S32647	parasporal crystal
40	820	24.1	1172	2 S32689	parasporal crystal
41	704	20.7	1380	2 B42459	hypothetical prote
42	677.5	19.6	1156	2 S19306	parasporal crystal
43	663	19.5	1136	1 USB581	parasporal crystal
44	626	18.4	934	1 B29838	parasporal crystal
45	617	18.1	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

A27323 parasporal crystal protein cry3aa1 - Bacillus thuringiensis

N:Alternate names: coleopteran-specific insect control protein; crystal protein cryC;

C/Species: Bacillus thuringiensis

C/Date: 19-Nov-1988 #sequence, revision 19-Nov-1988 #text-change 01-Dec-2000

C/Accession: A27323; A26853; A29987; A28407; S60781; I39812; I39813

R:Herrnstadt, C.; Gilroy, T.E.; Sobleski, D.A.; Bennett, B.D.; Gaertner, F.H.

Gene 57, 37-46, 1987

A:Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active

A:Reference number: A27323; MUID:88112860; PMID:2828180

A:Accession: A27323

A:Molecule type: DNA

A:Residues: 1-652 <HOB>

A:Cross-references: GB:M22472; NID:G142733; PIDN:AAA22336.1; PID:G142734

A:Experimental source: strain San Diego

R:Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.

Nucleic Acids Res. 15, 7183, 1987

A:Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus t

A:Reference number: A26853; MUID:88015559; PMID:3658680

A:Accession: A26853

A:Molecule type: DNA

A:Residues: 9-652 <HOB>

A:Cross-references: GB:Y00420; NID:940252; PIDN:CAA6482.1; PID:940253

A:Experimental source: var. tenebrionis

R:McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff,

Bio/Technology 6, 61-66, 1988

A:Title: Characterization of the coleopteran-specific protein gene of Bacillus thurin

A:Reference number: A29987

A:Accession: A29987

A:Molecule type: DNA

A:Residues: 9-652 <MCP>

A:Experimental source: var. tenebrionis

R:Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987

A:Title: Molecular cloning and characterization of the insecticidal crystal protein 9

A:Reference number: A28407

A:Accession: A28407

A:Molecule type: DNA

A:Residues: 9-652 <SRK>

A:Experimental source: var. Tenebrionis

R:Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.

Mol. Microbiol. 14, 381-389, 1994

A:Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized stra

A:Reference number: S60781; MUID:95131759; PMID:7830581

A:Accession: S60781

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-652 <ADA>

A:Cross-references: EMBL:U10985; NID:9506182; PIDN:MAC43266.1; PID:9514312

A:Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R.W., S.J.: Dean, D.H.
J. Mol. Biol. 255, 628-640, 1996
A:Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis
A:Reference number: 562317; MUID:96163555; PMID:8568902
A:Contents: annotation

R:Donovan, W.P.; Gonzalez, J.M.
Mol. Gen. Genet. 214, 365-372, 1998

A:Title: Isolation and characterization of Eg2158, a new strain of Bacillus thuringiensis
A:Reference number: 139812; MUID:89112139; PMID:3146015
A:Accession: 139812

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 9-652 <RES>
A:Cross-references: GB:M37207; NID:9142735; PIDN:AAA50255.1; PID:9142736

A:Experimental source: strain Eg2158
R: Teixeira de Souza, M.; Lecadet, M.M.; Lereclus, D.

J. Bacteriol. 175, 2952-2960, 1993
A:Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a

A:Reference number: 139813; MUID:93239393; PMID:8491716
A:Accession: 139813

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 9-58 <RES>
A:Cross-references: GB:I03393; NID:9304150; PIDN:AAA22350.1; PID:9551698

A:Gene: cryIIIA
A:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 100.0%; Score 3406; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 60
DB 9 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 68
QY 61 TTKDVIQKISVYDGLGVGPPFGALVSTYTNFNTWPSDEDPKAFMEQVEALMDOK 120
DB 69 TTKDVIQKISVYDGLGVGPPFGALVSTYTNFNTWPSDEDPKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLNQNNVEDYVSAISSMOKNPVSSRNPHSGRIRRELSQASHEFRNS 180
DB 129 IADYAKKALAELOGLNQNNVEDYVSAISSMOKNPVSSRNPHSGRIRRELSQASHEFRNS 188
QY 181 MPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 189 MPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 248
QY 241 DHCVKWYNGDLKLRGSSYESVWNNFRYRREMTLVLDLALFPLVYDRLVPRKYEKTELT 300
DB 249 DHCVKWYNGDLKLRGSSYESVWNNFRYRREMTLVLDLALFPLVYDRLVPRKYEKTELT 308
QY 301 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIOFHTRFQPGYGNDSFNWYS 360
DB 309 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIOFHTRFQPGYGNDSFNWYS 368
QY 361 GNYVSTRPSIGSNDLITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWP- 420
DB 369 GNYVSTRPSIGSNDLITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWP- 428
QY 421 KVEFSQYNDQTDDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 480
DB 429 KVEFSQYNDQTDDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 488
QY 481 MGSAGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVGAPFTGGDIIOC 540
DB 489 MGSAGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVGAPFTGGDIIOC 548
QY 541 TENGSAATITVTPDVSQKRYRARIHVASTQITFTLSDAPFNQYFEDTKINKGDTLT 600
DB 549 TENGSAATITVTPDVSQKRYRARIHVASTQITFTLSDAPFNQYFEDTKINKGDTLT 608

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QY 601 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 609 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 652

RESULT 2

parasporal crystal protein cry3cal - Bacillus thuringiensis subsp. kurstaki (strain B
N/alternat names: parasporal crystal protein cryIIID
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
C:Accession: JH0261; S18944
R: Lambert, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Se
Gene 110, 131-132, 1992

A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crys
A:Reference number: JH0261; MUID:92184108; PMID:1544571
A:Accession: JH0261

A:Molecule type: DNA

A:Residues: 1-649 <LAM>

A:Cross-references: EMBL:X59797; NID:940287; PIDN:CAA42469.1; PID:940288

A:Gene: cryIIID
A:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 75.3%; Score 2564.5; DB 1; Length 649;
Best Local Similarity 74.4%; Pred. No. 4.3e-161;
Matches 485; Conservative 63; Mismatches 93; Indels 11; Gaps 5;

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QY 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 58
QY 61 TTKDVIQKISVYDGLGVGPPFGALVSTYTNFNTWPSDEDPKAFMEQVEALMDOK 120
DB 59 TTKDVIQKISVYDGLGVGPPFGALVSTYTNFNTWPSDEDPKAFMEQVEALMDOK 118
QY 121 IADYAKKALAELOGLNQNNVEDYVSAISSMOKNPVSSRNPHSGRIRRELSQASHEFRNS 180
DB 119 IADYAKKALAELOGLNQNNVEDYVSAISSMOKNPVSSRNPHSGRIRRELSQASHEFRNS 178
QY 181 MPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 179 MPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 238
QY 241 DHCVKWYNGDLKLRGSSYESVWNNFRYRREMTLVLDLALFPLVYDRLVPRKYEKTELT 300
DB 239 DHCVKWYNGDLKLRGSSYESVWNNFRYRREMTLVLDLALFPLVYDRLVPRKYEKTELT 298
QY 301 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIOFHTRFQPGYGNDSFNWYS 360
DB 299 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIOFHTRFQPGYGNDSFNWYS 358
QY 361 GNYVSTRPSIGSNDLITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWP- 420
DB 359 GNYVSTRPSIGSNDLITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWP- 418
QY 416 YSGTQVEFSQYNDQTDDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 475
DB 419 YSGTQVEFSQYNDQTDDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 478
QY 476 YMCFLMGSGRTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVGAPFTGG 535
DB 479 YMCFLMGSGRTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVGAPFTGG 538
QY 536 DIIOCTENGSAATITVTPDVSQKRYRARIHVASTQITFTLSDAPFNQYFEDTKINKGDTLT 593
DB 539 DIIOCTENGSAATITVTPDVSQKRYRARIHVASTQITFTLSDAPFNQYFEDTKINKGDTLT 597
QY 594 NKGGTILYNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 598 NKGGTILYNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 649

```

RESULT 3

parapsoral crystal protein cry3Bb1 - *Bacillus thuringiensis*

N/Alternate names: parapsoral crystal protein cryIIIB2

C/Species: *Bacillus thuringiensis*

C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000

C/Accession: I39811

R/Donovan, W.P.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.H.

Appl. Environ. Microbiol. 58, 3921-3927, 1992

A/Title: Characterization of two genes encoding *Bacillus thuringiensis* insecticidal crys

A/Reference number: I39811; MUID:93119147; PMID:1476436

A/Accession: I39811

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-652 <RES>

A/Cross-references: GB:M89794; NID:q142729; PIDN:AAA2334.1; PID:q142730

C/Genetics:

A:Gene: cryIIIB2

C:Superfamily: parapsoral crystal protein

Query Match 68.7%; Score 2341.5; DB 2; Length 652;
Best Local Similarity 68.6%; Pred. No. 2,1e-146;
Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;

```

OY 1 MNPNNRSEHDTIKTTEENNEVPTNHVQPLAETPNPLEDLNKEFLRMADNTEALDSS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNPNNRSEHDTIKTTPNSELOTNHNQYPLADNPSTLEELNKEFLRMTEDESSTEVLDNS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 TTKDVIOKGISVVDLLGVGPPGALVSFYTNFLNTIWPSE-DPWKAFMEQVLEALMDQ 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TVKAVAGTGISVVGQILGVGVPFAGALTSFYOSFLNTIWPSDADPWKAFMAQVEVLIDK 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 KIDVYAKNKALAELOGLONNVEDYVSLSSWQKNPVSRRNPSSQGRITRELSQAESHFRN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KIEEYAKSKALAELOGLONNVEDYVSLSSWQKNPVSRRNPSSQGRITRELSQAESHFRN 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 180 SMPFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SMPFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 240 TDHCVMYNNVGLDKLSSYSESVNFRNRRREMTLVLDLALFPLVDVRLPKYKTEL 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TDHCVMYNNVGLDKLSSYSESVNFRNRRREMTLVLDLALFPLVDVRLPKYKTEL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 300 TRDLVTPDIVGNLKGVTFTSNIENYIRKPHLEDFYLRHQFTFRPOGYGNDSEFNW 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TRDLVTPDIVGNLKGVTFTSNIENYIRKPHLEDFYLRHQFTFRPOGYGNDSEFNW 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 360 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPDA-VYSG 418
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPDA-VYSG 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 419 VTKVEFSQYNDQDEASTQYDSKRNKVGAV-SMDSIDQLPPEETDEPLEKYSHQLNVM 477
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 VTKVEFSQYNDQDEASTQYDSKRNKVGAV-SMDSIDQLPPEETDEPLEKYSHQLNVM 480
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 478 CFMLQSGRGTIPVLTWTHKSVDFENMIDSKKITQLPLVYKAYKLGASVAVAPRFTGDI 537
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 CFMLQSGRGTIPVLTWTHKSVDFENMIDSKKITQLPLVYKAYKLGASVAVAPRFTGDI 540
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 538 IQCTE-NGSAATIVT-PDVSYSOKYRARIHYASTOITFLLSDGAFENQYFEDKTIK 595
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 LFLKSSNSIAKEFVTLNSAALLQRYRIRASTTNLRLEFVONSNDPLVYIINKTKNK 600
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 596 GDTLYNSFNLAFTPELSSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 643
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 DDDLTYQTFDLATNSNMNGSGDKNELIIGAESFVSNKTIYDKIEFIPV 650
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 4

parapsoral crystal protein cry3ba1 - *Bacillus thuringiensis* (fragment)

N/Alternate names: coleopterian-active parapsoral crystal protein; delta-endotoxin

C/Species: *Bacillus thuringiensis*

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000

C/Accession: S10228

R/Sick, A.; Gaertner, F.; Wong, A.

Nucleic Acids Res. 18, 1305, 1990

A/Title: Nucleotide sequence of a coleopterian-active toxin gene from a new isolate of

A/Reference number: S10228; MUID:90206811; PMID:2320431

A/Accession: S10228

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-659 <SIC>

A/Cross-references: EMBL:X17123; NID:g40258; PIDN:CAA3983.1; PID:g40259

C/Genetics:

A:Gene: cryIIIB

C:Superfamily: parapsoral crystal protein

C/Keywords: delta-endotoxin; toxin

Query Match 67.7%; Score 2307.5; DB 2; Length 659;
Best Local Similarity 68.0%; Pred. No. 3.8e-144;
Matches 442; Conservative 75; Mismatches 126; Indels 7; Gaps 6;

```

OY 1 MNPNNRSEHDTIKTTEENNEVPTNHVQPLAETPNPLEDLNKEFLRMADNTEALDSS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 MNPNNRSEHDTIKTTPNSELOTNHNQYPLADNPSTLEELNKEFLRMADNTEALDSS 68
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 TTKDVIOKGISVVDLLGVGPPGALVSFYTNFLNTIWPSE-DPWKAFMEQVLEALMDQ 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 TVKAVAGTGISVVGQILGVGVPFAGALTSFYOSFLNTIWPSDADPWKAFMAQVEVLIDK 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 KIDVYAKNKALAELOGLONNVEDYVSLSSWQKNPVSRRNPSSQGRITRELSQAESHFRN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 KIEEYAKSKALAELOGLONNVEDYVSLSSWQKNPVSRRNPSSQGRITRELSQAESHFRN 188
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 180 SMPFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 189 SMPFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 248
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 240 TDHCVMYNNVGLDKLSSYSESVNFRNRRREMTLVLDLALFPLVDVRLPKYKTEL 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 TDHCVMYNNVGLDKLSSYSESVNFRNRRREMTLVLDLALFPLVDVRLPKYKTEL 308
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 300 TRDLVTPDIVGNLKGVTFTSNIENYIRKPHLEDFYLRHQFTFRPOGYGNDSEFNW 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 309 TRDLVTPDIVGNLKGVTFTSNIENYIRKPHLEDFYLRHQFTFRPOGYGNDSEFNW 368
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 360 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPDA-VYSG 418
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPDA-VYSG 428
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 419 VTKVEFSQYNDQDEASTQYDSKRNKVGAV-SMDSIDQLPPEETDEPLEKYSHQLNVM 477
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 429 VTKVEFSQYNDQDEASTQYDSKRNKVGAV-SMDSIDQLPPEETDEPLEKYSHQLNVM 488
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 478 CFMLQSGRGTIPVLTWTHKSVDFENMIDSKKITQLPLVYKAYKLGASVAVAPRFTGDI 537
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 489 CFMLQSGRGTIPVLTWTHKSVDFENMIDSKKITQLPLVYKAYKLGASVAVAPRFTGDI 548
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 538 IQCTE-NGSAATIVT-PDVSYSOKYRARIHYASTOITFLLSDGAFENQYFEDKTIK 595
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 549 LFLKSSNSIAKEFVTLNSAALLQRYRIRASTTNLRLEFVONSNDPLVYIINKTKNK 608
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 596 GDTLYNSFNLAFTPELSSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 643
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 609 DDDLTYQTFDLATNSNMNGSGDTNDEIIGAESFVSNKTIYDKIEFIPV 658
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 5

cry465 protein - *Bacillus thuringiensis*

C/Species: *Bacillus thuringiensis*

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999

C/Accession: I40590

R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A:Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* tomocoids.

A:Reference number: I39814; MUID:95314293; PMID:7793960

A:Accession: I40590

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: EMBL:U07642; NID:g467234; PIDD:AAA82114.1; PID:g467235

A:Genetics:

A:Gene: cryV465

C:Superfamily: parasporal crystal protein

Query Match

Best Local Similarity 34.6%; Score 1178; DB 2; Length 719;

Matches 256; Conservative 132; Mismatches 234; Indels 42; Gaps 15;

```

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPPT---LEDLNYKKEFLMTADNNTA 56
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLLKNDKHOSLSNAKVDKISTDSLK-----NETDIELQNIHEDCLKMEYENP 50
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 LDSSTTKDVIYOKGISVVDLLGVGFPFGALVSPYTNFLNTIWP-SEDPKAKMEQVEA 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 IDPFVASTIQTGTIGIAGKILGTGLVPFAGQIASLSFLLGELMPKSKQMEIEMHEVE 110
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LMDOKIADYAKKALAELOGIANNVEDYVSAISSQKPNVSSRNPHSGRIREFLSQAES 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 IINOKITLYARKNALSLDRLGDLALAVYHDSLESWEN--RNNTARASVVKQYIALEL 167
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 HERNSPSFALISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEYKROLK 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MFVQKLPSPFVAVSGEVEPLPIYAQAANHLHLLDASIFGEMKLSSEISTFTFNROYER 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 TOEYDHCYKAVYNGGLDKLRGSSSVSWNENRNRREMTLVLDLALFPLYDVALPKREV 295
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 TRDYSDHCYKAVYNGGLDKLRGSSSVSWNENRNRREMTLVLDLALFPLYDVALPKREV 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 296 KTELTDVLDPIVGVNNLRGYGT-----FSNIE-NYIKRPHLDYLRHIOFH-- 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TSQLTREYVTDALGVHPQAFSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSL 347
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 -TRFQPGYGGNSFNWYSGNYSTRPSIGSDITSPFYGNKSSEPYQNLLENGEKYRA 402
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 LSRMSNTQY----NMWGGHKLREPRIGALNTSTOG-STNINSINP-VLQTSRDVYRT 401
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VANTNLAVPSPAVSGVTVVEFSQYNDQDEASTQYTD-SKRNVGAVSWDSIDQLPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 ESTLAGNLFLQTPVNGVPRVDHMKFPTLPRIASDNFYLGAGVGTQLDSENELPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 DEPLEKGYSHQNLNYVCMFLMGSRGTIPVLTWTHKSVDFENMIDSKKITQLPLVAKYKQ 521
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 GQPNVESYSHRLSHI--GLISASHVAKALVYSWTHRSADRTNTEPNSTIQPLVAFNLS 519
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 SCASVAVAGPRTGGDIIOCTENGSAATIVTPDVYSQYKRIARIHYASTSQITFTLSLDG 581
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 SCGAAYVAGPRTGGDIIRNTGTGFDIRVININPFAQRYRIRIVASTTDLQFHTSING 579
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 APFNQYFEDKTIKNGDILTYNSFNLSASTPELSS--NNLQIGVGLSAGDKVYIDKIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 KAINQGNFSATMNGEDLDYKTFRTIGFTTSPFSVDOSTFTIGAMNFSGNEVYIDRIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6

I39815

Insecticidal protein cryV - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999

C:Accession: I39815

R:Gleave, A.P.; Williams, R.; Hedges, R.J.

Appl. Environ. Microbiol. 59, 1683-1687, 1993
 A:Title: Screening by polymerase chain reaction of *Bacillus thuringiensis* serotypes f

lensis subsp. kurstaki.

A:Reference number: I39815; MUID:93298009; PMID:8517758

A:Accession: I39815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: GB:M08544; NID:g142767; PIDD:AAA22354.1; PID:g142768

A:Genetics:

A:Gene: cryV

C:Superfamily: parasporal crystal protein

Query Match

Best Local Similarity 33.9%; Score 1156; DB 2; Length 719;

Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

```

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPPT---LEDLNYKKEFLMTADNNTA 56
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLLKNDKHOSLSNAKVDKISTDSLK-----NETDIELQNIHEDCLKMEYENP 53
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 LDSSTTKDVIYOKGISVVDLLGVGFPFGALVSPYTNFLNTIWP-SEDPKAKMEQVEA 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 FVFAST---IQGTIGAKIILGTGLVPFAGQVASLSFLLGELMPKSKQMEIEMHEVE 110
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LMDOKIADYAKKALAELOGIANNVEDYVSAISSQKPNVSSRNPHSGRIREFLSQAES 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 IINOKITLYARKNALSLDRLGDLALAVYHDSLESWEN--RNNTARASVVKQYIALEL 167
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 HERNSPSFALISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEYKROLK 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MFVQKLPSPFVAVSGEVEPLPIYAQAANHLHLLDASIFGEMKLSSEISTFTFNROYER 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 TOEYDHCYKAVYNGGLDKLRGSSSVSWNENRNRREMTLVLDLALFPLYDVALPKREV 295
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 AGDYSYDHCYKAVYNGGLDKLRGSSSVSWNENRNRREMTLVLDLALFPLYDVALPKREV 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 296 KTELTDVLDPIVGVNNLRGYGT-----FSNIE-NYIKRPHLDYLRHIOFH-- 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TAQLTREYVTDALGVHPHPSFTSTWYNNAPSFSAIEAAVIRNPHLLDFLEQVTIYSL 347
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 -TRFQPGYGGNSFNWYSGNYSTRPSIGSDITSPFYGNKSSEPYQNLLENGEKYRA 402
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 LSRMSNTQY----NMWGGHKLREPRIGALNTSTOG-STNINSINP-VLQTSRDVYRT 401
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VANTNLAVPSPAVSGVTVVEFS-QYNDQDEASTQYTD-SKRNVGAVSWDSIDQLPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 ESTLAGNLFLQTPVNGVPRVDHMKFPTLPRIASDNFYLGAGVGTQLDSENELPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 DEPLEKGYSHQNLNYVCMFLMGSRGTIPVLTWTHKSVDFENMIDSKKITQLPLVAKYKQ 521
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 GQPNVESYSHRLSHI--GLISASHVAKALVYSWTHRSADRTNTEPNSTIQPLVAFNLS 519
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 SCASVAVAGPRTGGDIIOCTENGSAATIVTPDVYSQYKRIARIHYASTSQITFTLSLDG 581
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 SCGAAYVAGPRTGGDIIRNTGTGFDIRVININPFAQRYRIRIVASTTDLQFHTSING 579
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 APFNQYFEDKTIKNGDILTYNSFNLSASTPELSS--NNLQIGVGLSAGDKVYIDKIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 KAINQGNFSATMNGEDLDYKTFRTIGFTTSPFSVDOSTFTIGAMNFSGNEVYIDRIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

A48944

Parasporal crystal protein cry7Aa1 - *Bacillus thuringiensis*

N:Alternate names: parasporal crystal protein cry7iic

C:Species: *Bacillus thuringiensis*

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A48944

C:Accession: S25383
 R:Taylor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
 Mol. Microbiol. 6, 1211-1217, 1992
 A:Title: Identification and characterization of a novel *Bacillus thuringiensis* delta-end
 A:Reference number: S25383; MID:92269502; PMID:158820
 A:Accession: S25383
 A:Molecule type: DNA
 A:Residues: 1-719 <TAI>
 A:Cross-references: EMBL:X62821; NID:940289; PID:CAA44633.1; PID:940290
 C:Genetics:
 A:Gene: cryV
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 33.7%; Score 1147; DB 2; Length 719;
 Best Local Similarity 37.8%; Pred. No. 1.2e-67;
 Matches 251; Conservative 132; Mismatches 239; Indels 42; Gaps 15;

```

QY 1 MNRNRESDHTIKTTER-NEVPTNHVOYPLAETPPT---LEDLNYKEFLMTADNNTA 56
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1 MRLKNDKHQSFSSNAKVDKISTDSLK-----NETDIELQNIHEDCLKMSEYENVEP 53
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 57 LDSSTKDVYOKGISVVDLGVGFPFGALVSEYTNFLNTIMP-SEDPKAFMEQVEA 115
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 54 FVFAST---IQIGIGAKILGTLGVPPAGOVASLSFLLGELMPKGMQWELFMEHVEE 110
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 116 LMDOKIADYAKKALAELOGLQNNVEDYVSLSSMOKNPVSSRNPHSGRIREFSQAES 175
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 111 IINOKISTYARKKALTDKGLDALAVYHDSLESVGN--RNNTARASVYSQYIALLEL 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 176 HERNMSPFAISGVEVLFLTYAQAANTHLFLKDAQIYGEKGEYKEDIAPFYKROLK 235
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 168 MFVQKLPSEFVSGEEVPLPIYAQAANLHLLDASIFGEKGLSSSEISTEYFNQOVER 227
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 236 TOETDHCYKMYNGGLKRGSSSESVNENRYRREMTLVLDLALFPLYDVALREKVEY 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 228 AGDYSYHCYKMYSTGLNLRGTMASVWRYNQFRDMTLMVLDLALFPLYDVALREKVEY 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 296 KTELTDVLDPIYGVNRLRGYGT-----FSNIE-NYIKRPHLYLHRIQFH-- 343
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 288 TQALTREYTTALGIVHHPHSFTSTWYNNNAPEFSALIAAVVNPPLDLFLEQVYISL 347
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 344 -TRPOGYGNDSEFNWYSGVSTRPSIGSNDIITSPFYGNKSSSEPVQNLSENGEKYRA 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 348 LSRMSNTQY----MMMGHKLFR-TIGTLNISTGSGTNSINPV-TLPFTSRDYKRT 401
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 403 VANTNLAWPSAVYSGVTRVEFS-QYNDQIDEASTQYDSCRNGAVSWSIDQLPETT 461
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 402 ESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIASDNFYPGAGIGTQLODSENELPEAT 461
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 462 DEPLEKGYSHOANTVCMFLMOSRGITPVLTHKSVDFNMIDSKKITQDPLVAKYKIQ 521
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 462 GQPNYESHSLSHI--GLISASHVAKALVSWTHRSADRNTIEPNSITQDPLVAKFNLS 519
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 522 SGASVAVAGPREFGDIIOCTENGSAATIVTPDVYSOKYRARIHVASQTIFTLSDG 581
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 520 SGAIVVAGPFGTGGDILRTNTGTGDIRVNNPFAQRYRIRKASTITDIOFTTSING 579
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 582 APFNQYEDKTIKNGDILTNSEFLASFTPELSSG--NNLQIGVGLSAGDKYVYDKIE 639
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 580 KAIQGNFSATMNGEDLDYKTFRTVGFTTFPSFLDVQSTFTIGAMNFSGNEVYIDRIE 639
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 640 FIVP 643
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 640 FIVP 643
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 10

139814
 Insecticidal protein cryVI - *Bacillus thuringiensis*
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C:Accession: 139814

R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A:Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis*
 A:Reference number: 139814; MID:95314293; PMID:7793960
 A:Accession: 139814
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <RES>
 A:Cross-references: GB:L36338; NID:9540281; PID:AMC36999.1; PID:9540282
 C:Genetics:
 A:Gene: cryVI
 C:Superfamily: parasporal crystal protein

Query Match 33.7%; Score 1147; DB 2; Length 719;
 Best Local Similarity 37.8%; Pred. No. 1.2e-67;
 Matches 251; Conservative 132; Mismatches 239; Indels 42; Gaps 15;

```

QY 1 MNRNRESDHTIKTTER-NEVPTNHVOYPLAETPPT---LEDLNYKEFLMTADNNTA 56
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1 MRLKNDKHQSFSSNAKVDKISTDSLK-----NETDIELQNIHEDCLKMSEYENVEP 53
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 57 LDSSTKDVYOKGISVVDLGVGFPFGALVSEYTNFLNTIMP-SEDPKAFMEQVEA 115
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 54 FVFAST---IQIGIGAKILGTLGVPPAGOVASLSFLLGELMPKGMQWELFMEHVEE 110
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 116 LMDOKIADYAKKALAELOGLQNNVEDYVSLSSMOKNPVSSRNPHSGRIREFSQAES 175
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 111 IINOKISTYARKKALTDKGLDALAVYHDSLESVGN--RNNTARASVYSQYIALLEL 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 176 HERNMSPFAISGVEVLFLTYAQAANTHLFLKDAQIYGEKGEYKEDIAPFYKROLK 235
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 168 MFVQKLPSEFVSGEEVPLPIYAQAANLHLLDASIFGEKGLSSSEISTEYFNQOVER 227
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 236 TOETDHCYKMYNGGLKRGSSSESVNENRYRREMTLVLDLALFPLYDVALREKVEY 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 228 AGDYSYHCYKMYSTGLNLRGTMASVWRYNQFRDMTLMVLDLALFPLYDVALREKVEY 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 296 KTELTDVLDPIYGVNRLRGYGT-----FSNIE-NYIKRPHLYLHRIQFH-- 343
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 288 TQALTREYTTALGIVHHPHSFTSTWYNNNAPEFSALIAAVVNPPLDLFLEQVYISL 347
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 344 -TRPOGYGNDSEFNWYSGVSTRPSIGSNDIITSPFYGNKSSSEPVQNLSENGEKYRA 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 348 LSRMSNTQY----MMMGHKLFR-TIGTLNISTGSGTNSINPV-TLPFTSRDYKRT 401
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 403 VANTNLAWPSAVYSGVTRVEFS-QYNDQIDEASTQYDSCRNGAVSWSIDQLPETT 461
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 402 ESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIASDNFYPGAGIGTQLODSENELPEAT 461
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 462 DEPLEKGYSHOANTVCMFLMOSRGITPVLTHKSVDFNMIDSKKITQDPLVAKYKIQ 521
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 462 GQPNYESHSLSHI--GLISASHVAKALVSWTHRSADRNTIEPNSITQDPLVAKFNLS 519
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 522 SGASVAVAGPREFGDIIOCTENGSAATIVTPDVYSOKYRARIHVASQTIFTLSDG 581
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 520 SGAIVVAGPFGTGGDILRTNTGTGDIRVNNPFAQRYRIRKASTITDIOFTTSING 579
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 582 APFNQYEDKTIKNGDILTNSEFLASFTPELSSG--NNLQIGVGLSAGDKYVYDKIE 639
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 580 KAIQGNFSATMNGEDLDYKTFRTVGFTTFPSFLDVQSTFTIGAMNFSGNEVYIDRIE 639
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 640 FIVP 643
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 640 FIVP 643
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 11

500873
 parasporal crystal protein cryBa1 - *Bacillus thuringiensis* subsp. *thuringiensis*
 N:Alternate names: parasporal crystal protein cryA4
 C:Species: *Bacillus thuringiensis* subsp. *thuringiensis*
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000

C:Accession: S00873
 R:Brizard, B.L.; Whiteley, H.R.
 Nucleic Acids Res. 16, 2723-2724, 1988
 A:Title: Nucleotide sequence of an additional crystal protein gene cloned from *Bacillus*
 A:Reference number: S00873; MUID:88203216; PMID:3362680
 A:Accession: S00873
 A:Molecule type: DNA
 A:Residues: 1-1228

 A:Cross-references: EMBL:X06711; NID:940264; PIDN:CAA29698.1; PID:9580949
 A:Gene: cryA4
 A:Start codon: TTTG
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 32.6%; Score 1109; DB 2; Length 1228;
 Best Local Similarity 38.3%; Pred. No. 9.1e-65;
 Matches 236; Conservative 116; Mismatches 237; Indels 60; Gaps 22;

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OY 1 MNPNNRSEHDTIKTENNEVPNNHVOYPLAETPNPLEDLNKEFLRMTADNTEALDSS 60
DB 1 MTSNRKRENTIINAVSHSAMD-----LLPDARIEDSLCIAEGNNIDPEVSA 48
OY 61 TTRDVIQKGISVVGDLGVGFPFGALVSPYTNELTTP--SEDPKAFMEQVEALMDQ 119
DB 49 ST---VGTGINGRIIGLVGVPFAGQLASFYSFLVGLMPPRGDRDWELEFLEHVEOLIQ 105
OY 120 KINDYAKNKALAELOGIANNVEDYVALSSMOKKPVSSRNPDSGRIRE-LFSQ---AES 175
DB 106 QITENANNTALARIQAGDSFRAIQSLEDMLEN-----RDDAKRSVLYQYIALLEL 158
OY 176 HFRNSMPSFAISGVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFPKROLK 235
DB 159 DELNAMPLEAIRNQEVEFLMAYQAANLHLLLDASLFGSEFGLTQEIQRERYEQR 218
OY 236 TOEYTHCHVKRYNGLDLKGSSESVNPKRYREMTLYVDLIAFPFLYDLVLYRKEV 295
DB 219 TRDSDVCVEWYNTGLNSLRGTNAAWRYNQFRDLGLVLDLVALPSTIDNTYPIINT 278
OY 296 KTELRLDVLDPDPI--VGVN--NLRGYGT--TFSNIE-NYIRKPHLFDYLHRIQFHTRFQ 347
DB 279 SAQLTREYVTAIGATGVNMAAMNNAPSFSAIEAARSHLDLDFLEQLITFSA-S 337
OY 348 PGYGNDSFNWYSGNVYSTRPSIGSNDITTSPEYG--NKSEPVQNLPEKCEKRYAVAN 405
DB 338 SRMSSTRIMTYRNGHTIQSRP--IGGG--LNTSTGATWTSINPY-TLRFASRDYRRESY 393
OY 406 TNLAVWPSAVY-----SGVTKEFSGOYNDQ--TDEAS--TQTYDSKRNVGAVMSDSIDL 456
DB 394 AGVLLW--GILEPIHGVPIVRFNFTNPONISDKGTANYSQPYESP--GLQLKDSFTEL 448
OY 457 PPEITDEPLEKGYSHQNLVYVCFMLOGSRGTIPVLTWTHKSVDFENMIDSKKITQLPLVK 516
DB 449 PPEITERNNYESYSHRSHIGILQ--SRVNVVYVSMTHRADRNITIGPRITQIPMK 506
OY 517 AVKIOGASVVAAPRFTGDIIOCTENGSAATITTPPVSVSQKRAIHVASTQITFT 576
DB 507 ASELPGQTTVAVGPGFTGDIIRNTGFGFGRIVTNGPLTORIRIGFRRASTVDEDF 566
OY 577 LSLDGAPENOYVFDKTIKNGDPLTNSFNLSFSPPEELS--GNMLQIGVTLGSLAGDYV 634
DB 567 VSRGTTVNNRFLRTMNSGDELAKGNFYRAFTTPTFTQLODLIRISIGLSONGEVY 626
OY 635 IDKIEFIPV 643
DB 627 IDKIEFIPV 635

```

RESULT 12
 I40589
 parasporal crystal protein cry8Cal - *Bacillus thuringiensis*
 N:Alternate names: parasporal crystal protein cryIIII
 C:Species: *Bacillus thuringiensis*

C:Date: 12-Aug-1996 #sequence-revision 12-Aug-1996 #text-change 01-Dec-2000
 C:Accession: I40589
 R:Sato, R.; Takeuchi, K.; Ogihara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Horii, H.; As
 Curr. Microbiol. 28, 15-19, 1994
 A:Title: Cloning, heterologous expression, and localization of a novel crystal protei
 A:Reference number: I40589; MUID:94100786; PMID:7764305
 A:Accession: I40589
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1160 <RES>
 A:Cross-references: EMBL:U04366; NID:9532523; PIDN:AAA21119.1; PID:9532524
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 30.4%; Score 1034.5; DB 2; Length 1160;
 Best Local Similarity 35.4%; Pred. No. 6.7e-60;
 Matches 247; Conservative 124; Mismatches 235; Indels 91; Gaps 24;

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OY 1 MNPNNRSEHDTIKTENNEVPNNHVOYPLAETPNPLEDLNKEFLRMTADNTEALDSS 60
DB 1 MNPNNRSEHDTIKTENNEVPNNHVOYPLAETPNPLEDLNKEFLRMTADNTEALDSS 60
OY 61 TTRDVIQKGISVVGDLGVGFPFGALVSPYTNELTTPS--EDPKAFMEQVE 114
DB 61 GFTISQADAVGICIDIVSTIIISGLIPVLGEVFSILGSLGLMPSNNENWQIMNRYE 120
OY 115 ALMDQRIADYAKNKALAELOGIANNVEDYVALSSMOKKPVSSRNPDSGRIRELFSAE 174
DB 121 ELIDQKILDSVSRALADLANSRIAYEQNALDEMRKNPHSTR--SAALKEFRFGNE 177
OY 175 SHRNSMPSFAISGVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFPKROLK 234
DB 178 ALIRTNMGSQSNYETTPLEPTIQAANSLHLVLRDVOYIGKEWGPONDIDLFREQVS 237
OY 235 LTOEYTHCHVKRYNGLDLKGSSESVNPKRYREMTLYVDLIAFPFLYDLVLYRKEV 294
DB 238 YTRARYSDHCQWYVAGLNLKRGAKOWDYNNFRMMVAVLDLVALPPNDARYPLE 297
OY 295 VKTELRLDVLDPDPI--VGVN--NLRGYGT--TFSNIE-NYIRKPHLFDYLHRI 340
DB 298 TNLRLREITPDV--GSVYTGQSTLISWYDMIPALPSFTLENLKRKPDFTILOEI 355
OY 341 QPHTRFPQ---YGNDSFNWYSGNVYSTRPSIGSNDITTSPEYGNKSSSEPV--ONLEP 394
DB 356 RMTSPFQNGTIEY-----NYNGGQRLTSTLYGSSFNKYSGLAGADIIPVGN--- 407
OY 395 NGEKRYRAV-----ANTNLAVWPSAVYSGVTKEFSGOYNDQTDASOTQTFDKRNV-- 445
DB 408 ---DIYRVWYTIIGRYTNSILGVNVPVTFY-----FSNNTQ---KYSKPKQFAG 450
OY 446 GAVMSDSIDLPEPITDEPLEKGYSHQNLVYVCFMLOGSRGT---IPVLTWTHKSVDFE 501
DB 451 GIKTIIDGEEETLEN-----YQSTSHRVSYITSEIKSTGIVLGVVPIGWTHSSASRN 505
OY 502 NMIDSKKITQLPLVKAYKIOSGA--SVVAGPRFTGDIIOCTENGSAATITTPPV--SY 557
DB 506 NFYATATISQIPKIKASRTSGGAVWNNQEG--LVNGCPWMLSSGSGOYVNLRVATDAGA 564
OY 558 SQKTRARIHASTQITFTLSLDAEPN-----QYFEDTKINKGDTLTNSFNLSFST 611
DB 565 SQRIRIRIRVASDAGKFTIS--SRSPENPATYSASIAVYTMSTNSLVYSTEAVAE--SG 622
OY 612 PFEI-----SCNNLQIGVTLGSLAGDYIDKIEFIPV 644
DB 623 PINLGSSSKRTFIDISTIKKAGANLYIDRIEFLPV 659

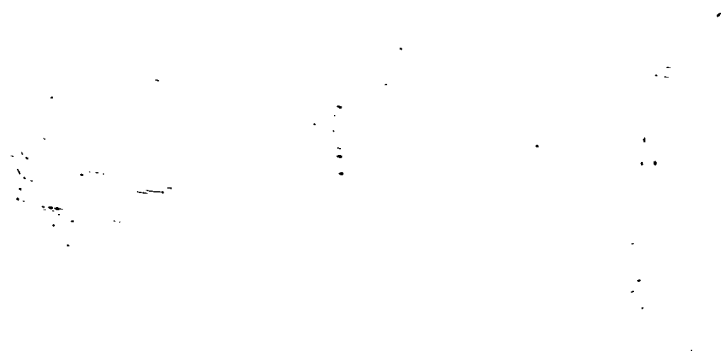
```

RESULT 13
 S39536
 parasporal crystal protein cry9Ba1 - *Bacillus thuringiensis*
 N:Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
 C:Species: *Bacillus thuringiensis*
 C:Date: 07-Oct-1994 #sequence-revision 01-Dec-1995 #text-change 01-Dec-2000

RESULT 14
A26513
parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai)
C:Species: *Bacillus thuringiensis*
C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 01-Dec-2000
C:Accession: A26513
R:Oda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
Gene 53, 113-119, 1987
A:Title: Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis*
A:Reference number: A26513; MUID:87248103; PMID:3297927
A:Accession: A26513

[illegible]

RESULT 15
 JD0002
 parasporeal crystal protein crystal3 - *Bacillus thuringiensis*
 N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal
 C:Species: *Bacillus thuringiensis*
 C:Date: 28-Dec-1987 #sequence:revision 28-Dec-1997 #text:change 01-Dec-2000
 C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
 R:Kondo, S.; Tamura, N.; Kunikida, A.; Hatiori, M.; Akashi, A.; Ohmori, I.
 A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes
 A:Reference number: A90025
 A:Accession: A90025
 A:Molecule type: mRNA



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 10:45:44 : Search time 14 Seconds

(without alignments)
1907.911 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406

Sequence: 1 MNPNNRSEHDRIKTEENNEV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	100.0	644	1 C3AA_BACTT	P07130 bacillus th
2	2564.5	75.3	649	1 C3CA_BACTK	Q45744 bacillus th
3	2341.5	68.7	652	1 C3BB_BACTU	Q06117 bacillus th
4	2307.5	67.7	659	1 C3BA_BACTO	P17969 bacillus th
5	1240	36.4	1157	1 C8AA_BACUK	Q45704 bacillus th
6	1187	34.9	1169	1 C8BA_BACUK	Q45705 bacillus th
7	1178	34.6	719	1 C1B_BACTE	Q45709 bacillus th
8	1176.5	34.5	719	1 C1ID_BACTU	Q9X411 bacillus th
9	1174.5	34.5	1138	1 C7AB_BACUK	Q45708 bacillus th
10	1159.5	34.0	1138	1 C7AB_BACUA	Q45707 bacillus th
11	1156.5	34.0	1229	1 C1BB_BACTU	Q45739 bacillus th
12	1156.5	34.0	1233	1 C1BC_BACTM	Q45774 bacillus th
13	1156	33.9	719	1 C1IA_BACTK	Q45752 bacillus th
14	1152.5	33.8	1138	1 C7AA_BACTU	Q03749 bacillus th
15	1149	33.7	1157	1 C9CA_BACTO	Q45733 bacillus th
16	1141	33.5	1169	1 C9DA_BACTP	Q06014 bacillus th
17	1130.5	33.2	1215	1 C1KA_BACTM	Q45715 bacillus th
18	1109	32.6	1228	1 C1BA_BACTK	P05517 bacillus th
19	1090	32.0	719	1 C1IC_BACTU	Q87404 bacillus th
20	1063.5	31.2	1227	1 C1BE_BACTU	Q85805 bacillus th
21	1044.5	30.7	1150	1 C9EA_BACTA	Q9Zn19 bacillus th
22	1034.5	30.4	1231	1 C8CA_BACTP	Q45706 bacillus th
23	1030.5	30.3	1231	1 C1BD_BACTZ	Q9Za25 bacillus th
24	1012.5	29.7	1163	1 C0AA_BACMF	Q9X597 bacillus th
25	980	28.8	1155	1 C1AB_BACTK	P06578 bacillus th
26	971.5	28.5	1181	1 C1AE_BACTL	Q03748 bacillus th
27	970	28.5	1179	1 C1AD_BACTA	Q03744 bacillus th
28	944.5	27.7	1189	1 C1CA_BACTE	P05518 bacillus th
29	938.5	27.6	1176	1 C1AA_BACTG	P02965 bacillus th
30	929.5	27.3	1176	1 C1CB_BACTG	P69653 bacillus th
31	926	27.2	1170	1 C1JB_BACTM	Q45716 bacillus th
32	920	27.0	1169	1 C1GB_BACTZ	Q9Za26 bacillus th
33	911.5	26.8	1166	1 C1GA_BACTU	Q45746 bacillus th

34	908.5	26.7	1167	1 C1JA_BACTU	Q45738 bacillus th
35	883.5	25.9	911	1 C1AF_BACTU	P96315 bacillus th
36	883.5	25.9	1174	1 C1FA_BACTA	Q03746 bacillus th
37	883	25.9	1171	1 C1EA_BACTX	Q57458 bacillus th
38	882	25.9	1169	1 C1FB_BACTM	Q66377 bacillus th
39	860.5	25.3	1174	1 C1EB_BACTA	Q03745 bacillus th
40	859.5	25.2	1176	1 C1AG_BACTU	Q98515 bacillus th
41	852	25.0	1165	1 C1DA_BACTA	P19415 bacillus th
42	845.5	24.8	1178	1 C1AC_BACTK	P50068 bacillus th
43	835.5	24.5	1160	1 C1DB_BACTU	Q45747 bacillus th
44	828	24.3	1155	1 C1HB_BACTM	Q45718 bacillus th
45	820	24.1	1172	1 C1HA_BACTU	Q45748 bacillus th

ALIGNMENTS

RESULT 1
ID C3AA_BACTT STANDARD: PRT: 644 AA.
AC P07130; P21255;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry3A precursor (insecticidal delta-endotoxin CryIIIA(a)) (crystalline entomocidal protoxin) (73 kDa crystal protein).
GN CRY3AA OR CRYIIIA(A) OR CRYIIIA OR CRY3A OR CRYC OR BT13.
OS Bacillus thuringiensis (subsp. tenebrionis).
OS Bacillus thuringiensis (subsp. morrisoni), and
OS Bacillus thuringiensis (subsp. san diego).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1444, 1441, 1435;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=88015559; PubMed=3658680;
RA Hoeft H., Seuring J., Houtven A.V., Vaack M.;
RT "Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
RL Nucleic Acids Res. 15:7183-7183(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
RT "Molecular cloning and characterization of the insecticidal crystal protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B., Fischhoff D.A.;
RT "Characterization of the coleopteran-specific protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Biotechnology 6:61-66(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis; STRAIN=NB176;
RX MEDLINE=9511759; PubMed=7830581;
RA Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
RT "Elucidation of the mechanism of CryIIIA overproduction in a mutant strain of Bacillus thuringiensis var. tenebrionis.";
RL Mol. Microbiol. 14:381-389(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morrisoni; STRAIN=EG2158;
RX MEDLINE=89112139; PubMed=3146015;
RA Donovan W.P., Gonzalez J.M., Jr., Gilbert M.P., Dankocsk C.C.;
RT "Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis toxic to coleopteran larvae, and nucleotide sequence of the toxin gene.";
RL Mol. Gen. Genet. 214:365-372(1988).

RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.san diego;
 RA MEDLINE=88112860; PubMed=2828180;
 RX Hermsdorf C., Gilroy T.E., Sobleski D.A., Bennett B.D.,
 RA Gaertner F.H.;
 RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
 active delta-endotoxin gene from *Bacillus thuringiensis* subsp. *san*
 RT diego.";
 RL Gene 57:37-46(1987).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC SPECIES=B.t. tenebrionis;
 RX MEDLINE=92049729; PubMed=1658659;
 RA Li J., Carroll J., Ellar D.J.;
 RT "Crystal structure of insecticidal delta-endotoxin from *Bacillus*
 RT *thuringiensis* at 2.5-A resolution.";
 RL Nature 353:815-821(1991).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- BIOCHEMISTRY: Introduced by genetic manipulation and expressed in
 CC insect-resistant potato by Monsanto.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC
 CC EMBL: Y00420; CAA68482.1; -
 CC EMBL: J02978; AAA22561.1; -
 CC EMBL: M37207; AAA50295.1; -
 CC EMBL: U10985; AAC43266.1; -
 CC EMBL: M20503; AAA22542.1; -
 CC EMBL: M22472; AAA22336.1; ALF_INIT.
 CC PIR: A26853; A26853.
 CC PIR: A28407; A28407.
 CC PIR: A29987; A29987.
 CC PIR: A27323; A27323.
 CC PDB: IDLC; 30-SEP-94.
 CC InterPro: IPR001178; Endotoxin.
 CC Pfam: PF00555; endotoxin; 1.
 CC Toxin: Sporulation; 3D-structure: Genetically modified food.
 CC FT PROPEP 1 57 REMOVED IN MATURE FORM.
 CC CHAIN 58 644 PESTICIDIAL CRYSTAL PROTEIN CRY3AA.
 CC CONFLOC 544 544 G->A (IN REF. 3).
 CC SEQUENCE 644 AA; 73108 MW; EECFICEFD9683 CRC64;
 SQ
 Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.3e-216;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MNPNNRSEHDITKTENNEVPTNHQVPLAETPNPTLEDLNYKEFLRMTADNTEALDSS 60
 Db 1 MNPNNRSEHDITKTENNEVPTNHQVPLAETPNPTLEDLNYKEFLRMTADNTEALDSS 60
 Oy 61 TTKVOIGISVGDGLGVGFPFGGALVSFTYNTPLNTWSEDPWKAEMQVEALMDOK 120
 Db 61 TTKVOIGISVGDGLGVGFPFGGALVSFTYNTPLNTWSEDPWKAEMQVEALMDOK 120
 Oy 121 IADYAKNKALELOGLONNVEDYVSASSMQKNVSSRNPSQCRIRIELPSQASSHRNS 180
 Db 121 IADYAKNKALELOGLONNVEDYVSASSMQKNVSSRNPSQCRIRIELPSQASSHRNS 180
 Oy 181 MPSPALSGEVLFLTYAAQANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKTQDEYT 240

Db 181 MPSPALSGEVLFLTYAAQANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKTQDEYT 240
 Oy 241 DHCVKYNVGLDKLRSSYESVWNNRRYRRENTLVLDLALFPYDRLPKREKTELT 300
 Db 241 DHCVKYNVGLDKLRSSYESVWNNRRYRRENTLVLDLALFPYDRLPKREKTELT 300
 Oy 301 RQVLDPIYGVNNLNGYGTTFENIENYIRKPLFLYLRHQPHRFPQGYGNSFNWYS 360
 Db 301 RQVLDPIYGVNNLNGYGTTFENIENYIRKPLFLYLRHQPHRFPQGYGNSFNWYS 360
 Oy 361 GNYVSTRSIGSDNITTSPTFNKSSPEVONLEFNGEYVAVANTNLVPSAVSYGT 420
 Db 361 GNYVSTRSIGSDNITTSPTFNKSSPEVONLEFNGEYVAVANTNLVPSAVSYGT 420
 Oy 421 KYEFSQYNDQDEASTQYDYSKRNVAWSMDIDLPETDEPLEKGYSHQLVNMFCL 480
 Db 421 KYEFSQYNDQDEASTQYDYSKRNVAWSMDIDLPETDEPLEKGYSHQLVNMFCL 480
 Oy 481 MGSRGITPVLTWTHKSVDFPMIDSKKITQLPLVKAKKLOGSASVAGPRTGDIIOC 540
 Db 481 MGSRGITPVLTWTHKSVDFPMIDSKKITQLPLVKAKKLOGSASVAGPRTGDIIOC 540
 Oy 541 TENGSAATITVYPDVYSQKRYRARIHYASTQITFTSLDGAPPNOYFPDKTINKGDTLT 600
 Db 541 TENGSAATITVYPDVYSQKRYRARIHYASTQITFTSLDGAPPNOYFPDKTINKGDTLT 600
 Oy 601 YNSFNLASFSTPFELSGNNLDIGYTGASGDKYTIKIEFIPVN 644
 Db 601 YNSFNLASFSTPFELSGNNLDIGYTGASGDKYTIKIEFIPVN 644
 RESULT 2
 C3CA_BACTK STANDARD: PRT; 649 AA.
 AC 045744;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry3Ca (insecticidal delta-endotoxin
 DE CryIIIC(a)) (crystalline entomocidal protoxin) (73 kDa crystal
 DE protein).
 GN CRY3CA OR CRYIIIC(A) OR CRYIIID.
 OS *Bacillus thuringiensis* (subsp. *kurstaki*).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Br1109P;
 RX MEDLINE=92184108; PubMed=1544571;
 RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,
 RA Janssens S., Steurink J., Peferoen M.;
 RT "Nucleotide sequence of gene cryIIID encoding a novel coleopteran-
 RT active crystal protein from strain Br1109P of *Bacillus thuringiensis*
 RT subsp. *kurstaki*.";
 RL Gene 110:131-132(1992).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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DR EMBL: X59797: CAA42469.1: -
 DR HSSP: P07130: IDIC
 DR InterPro: IPR001178: Endotoxin.
 DR Pfam: PF00555: endotoxin.1.
 DR Toxin: Sporulation.
 KW SEQUENCE 649 AA: 73026 MW: 88FLF0B47957AC49 CRC64:

Query Match 75.3% Score 2564.5: DB 1: Length 649;
 Best Local Similarity 74.4%: Pred. No. 38-161;
 Matches 465: Conservative 63: Mismatches 93: Indels 11: Gaps 5;

1 MNPNNRSEHDTIKTENNEPTNHNVOYPLAETNPPTLEDLNTYKEFLRMADNTTEALDSS 60
 1 MNPNNRSEHDTIKTENNEPTNHNVOYPLAETNPPTLEDLNTYKEFLRMADNTTEALDSS 58
 61 TTKDVIOKGISVVDGLGVGPPGALVSFTYNTPLNTIPSPDPMKAFMEQVEALMDOK 120
 59 TTKDAIOKGISIGDILGVGPPGALVSFTYNTPLNTIPSPDPMKAFMEQVEALMDOK 118
 121 IADYAKKALAELOGIANNVEDYVSALSSWQKNPVSRRPHSOGRIREFLSQASHFRNS 180
 119 IADYAKKALAELOGIANNVEDYVSALSSWQKNPVSRRPHSOGRIREFLSQASHFRNS 178
 181 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLOEY 240
 179 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLOEY 238
 241 DHCYKWNVGLDKLRGSSYEWNNENRYRREMTLVLDLALFPYLDVRLYKREYKTEL 300
 239 NHCAKWKAKGIDLRGSTEYEWKFNRYRREMTLVLDLALFPYLDVRLYKREYKTEL 298
 301 RDVLTDPYGVNNLRGTYGTFENIENYIRKPHLEFDYLRHIOFHTPOPGYNDSEFNWYS 360
 299 RDVLTDPYGVNNLRGTYGTFENIENYIRKPHLEFDYLRHIOFHTPOPGYNDSEFNWYS 358
 361 GNYVSTRPSIGSNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAY 415
 359 GNYVSTRPSIGSNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAY 418
 416 YSGVTKEFSGNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAY 475
 419 HSGVTKEFSGNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAY 478
 476 VMCELMGSGRTIPVLTWTHKSVDFENMIDSKKITQOLPYKAYKLGSGASVYAGPRTGG 535
 479 VRCELMGSGRTIPVLTWTHKSVDFENMIDSKKITQOLPYKAYKLGSGASVYAGPRTGG 538
 536 DIIOCTENGSAATYV--PVSYSOKYRAIINASTSQTIFTLSDGAPPNQYEPDKTI 593
 539 DIIOCTENGSAATYV--PVSYSOKYRAIINASTSQTIFTLSDGAPPNQYEPDKTI 597
 594 NKGDITFNSFNLSFSTPELS--GNMLQIGVTGLSAGDKYIYDKIEFIPVN 644
 598 DKGNITFNSFNLSFSTPELS--GNMLQIGVTGLSAGDKYIYDKIEFIPVN 649

RESULT 3
 C3BB_BACTU STANDARD: PRT: 652 AA.

DR 30-MAY-2000 (Rel. 39, Created)
 DR 30-MAY-2000 (Rel. 39, Last sequence update)
 DR 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidicidal crystal protein cry3bb (insecticidal delta-endotoxin
 DE CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa crystal
 DE protein).
 GN CRY3BB OR CRYIIIB(B) OR CRYIIIB2.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1428;
 RN SEQUENCE FROM N.A.
 RP STRAIN=EG4961.

RA MEDLINE-93119147: PubMed-1476436;
 RA Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke M.C.,
 RA Johnson T.B.;
 RT "Characterization of two genes encoding Bacillus thuringiensis
 RT insecticidal crystal proteins toxic to Coleoptera species.";
 RL Appl. Environ. Microbiol. 58:3921-3927(1992).
 (2)

RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18655 / EG5144;
 RA Donovan W.P., Rupar M.J., Slaney A.C.;
 RT "Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran
 RT insects.";
 RT Patent number US5378625, 03-JAN-1995.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDDLE
 CC EPITHELIAL CELLS OF COLEOPTERA. HAS MODERATE LEVEL OF TOXICITY TO
 CC SOUTHERN CORN ROOTWORM.

CC -1- SUBUNIT: MONOMER.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC or send an email to license@isb-sdb.ch).

CC EMBL: M89794: AAA2334.1: -
 DR EMBL: U31633: AAA74198.1: -
 DR HSSP: P07130: IDIC.
 DR InterPro: IPR001178: Endotoxin.
 DR Pfam: PF00555: endotoxin.1.

KW Toxin: Sporulation.
 FT VARIANT 21 Q -> P (IN STRAIN EG5144).
 FT VARIANT 97 N -> D (IN STRAIN EG5144).
 FT VARIANT 289 I -> V (IN STRAIN EG5144).
 FT VARIANT 352 F -> S (IN STRAIN EG5144).
 FT VARIANT 417 VYL -> IYF (IN STRAIN EG5144).
 FT VARIANT 451 S -> G (IN STRAIN EG5144).
 FT VARIANT 590 L -> I (IN STRAIN EG5144).
 FT VARIANT 600 K -> I (IN STRAIN EG5144).
 FT VARIANT 624 K -> T (IN STRAIN EG5144).
 SQ SEQUENCE 652 AA: 74385 MW: 63048332CDE8CC6 CRC64:

Query Match 68.7% Score 2341.5: DB 1: Length 652;
 Best Local Similarity 68.6%: Pred. No. 14e-146;
 Matches 446: Conservative 75: Mismatches 122: Indels 7: Gaps 6;

1 MNPNNRSEHDTIKTENNEPTNHNVOYPLAETNPPTLEDLNTYKEFLRMADNTTEALDSS 60
 1 MNPNNRSEHDTIKTENNEPTNHNVOYPLAETNPPTLEDLNTYKEFLRMADNTTEALDSS 60
 61 TTKDVIOKGISVVDGLGVGPPGALVSFTYNTPLNTIPSPDPMKAFMEQVEALMDOK 119
 61 TTKDVIOKGISVVDGLGVGPPGALVSFTYNTPLNTIPSPDPMKAFMEQVEALMDOK 120
 120 KIDYAKKALAELOGIANNVEDYVSALSSWQKNPVSRRPHSOGRIREFLSQASHFRNS 179
 121 KIDYAKKALAELOGIANNVEDYVSALSSWQKNPVSRRPHSOGRIREFLSQASHFRNS 180
 181 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLOEY 239
 181 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLOEY 240
 240 TDHCYKWNVGLDKLRGSSYEWNNENRYRREMTLVLDLALFPYLDVRLYKREYKTEL 299
 241 TDHCYKWNVGLDKLRGSSYEWNNENRYRREMTLVLDLALFPYLDVRLYKREYKTEL 300

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QY 300 TRDVLTPDIYGVNNLRGTYGTFESNIENYIRKPHLEFDYLRHIOFHTROPQGYGNDSENYM 359
DB 301 TRDFTDPIFSLMLQEGPFLSEIENIRKPHLEFDYLRHIOFHTROPQGYGNDSENYM 360
QY 360 SGNVSTPSPISGNDITSPFYGKSEPVONLEFNGEKYRAVANINLAWPASA-VYSG 418
DB 361 SGNVSTPSPISGNDITSPFYGKSEPVONLEFNGEKYRAVANINLAWPASA-VYSG 420
QY 419 VTKVEFSQYNDQDEASTQYDYSKRNVAAS-NDSDIDQLPETTDEPLEGYSHQNLNYM 477
DB 421 VTKVEFSQYNDQDEASTQYDYSKRNVAAS-NDSDIDQLPETTDEPLEGYSHQNLNYM 480
QY 478 CFLMDSRGRTIPVLTWTHKSVDFPNMDSKRTIQLPVKAYKLSQASVAVAGPRTGDI 537
DB 481 CFLMDSRGRTIPVLTWTHKSVDFPNMDSKRTIQLPVKAYKLSQASVAVAGPRTGDI 540
QY 538 IQCTE-NGSAAITIVT-PDVSYSQKRYARIRHIVASTQITFTLSLDGAPNOYFDTINK 595
DB 541 LFLKSSNSIAKPKRYLNSAALLQRYRVRIRASTTNLEFVONSNDLVIYINKTMK 600
QY 596 GDTLTYSFNLASFSTPELGS--NNLQIGVTGLSAGDKVYIDKIEFIV 643
DB 601 DGDLTGTFTPATNSNMFGSGDNDIIGAESFVNEKIYIDKIEFIV 650

RESULT 4
ID C3BA_BACTO STANDARD; PRT; 659 AA.
AC F17969;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry3Ba (Insecticidal delta-endotoxin
DE CryIIIBa) (Crystalline entomocidal protoxin) (75 kDa crystal
DE protein).
GN CRY3BA OR CRYIIIB(A) OR CRYIIIB.
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RX NCBI_Taxid-1442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-43F;
RA MEDLINE-9020611; PubMed-2320431;
RA Sick A., Gaertner F.H., Wong A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi."
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL: X17123; CAA34983.1; -
DR EMBL: A07234; CAA00645.1; -
DR PIR: S10228; S10228.
DR HSSP: P07130; IDLC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
DR Toxin: Sporulation.
SQ SEQUENCE 659 AA; 75159 MW; 5A5B21AFF84168CA CRC64;

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Query Match          67.7%; Score 2307.5; DB 1; Length 659;
Best Local Similarity 68.0%; Pred. No. 2.4e-144;
Matches 442; Conservative 75; Mismatches 126; Indels 7; Gaps 6;

QY 1 MNPNNSEHDITKTENNEPPTNHVQYPLAEPNPTLEADNKEFLRMTADNNFALSS 60
DB 9 MNPNNSEVDITKVPNSLPTNHQYPLADNPNTLELNKKEFLRMTADNNSTEVLSS 68
QY 61 TTKDVIQAKISVYDGLGVGFPFGALVSEYTNFLNTWPS- DPWKAFFEYQALMDQ 119
DB 69 TVKDAVGTGISVVGQILGVYGVFPAGALTSFYQSEFLNIMPSPDAPKMAFAQYEVLDK 128
QY 120 KIADYAKNKAELQGLONNVEDYVSAALSSMQKNVSSRNHSGRIEELSQAESHFRN 179
DB 129 KIEEYAKSALAEGLQONNEDYVNAALSSMQKAVNLRSSRDRIRELPSQAESHFRN 188
QY 180 SMPFAISGEVFLFTTYAQAANTHFLPKDAQIYGEEMGEKEDIAPFYRQAKLQY 239
DB 189 SMPFAVSKFEVFLPTTYAQAANTHLLKDAQYGEEMGSSEDIAEFTYRQAKLQY 248
QY 240 TDHCYKKNVNGDLKRGSSYESWVNFRRREMTLVLDLALPPLVDRLYPREVTET 299
DB 249 TDHCYKKNVNGVLSLRSSTYDAWKFNRFRREMTLVLDLALPPLVDRLYSKGVKTEL 308
QY 300 TRDVLTPDIYGVNNLRGTYGTFESNIENYIRKPHLEFDYLRHIOFHTROPQGYGNDSENYM 359
DB 309 TRDFTDPIFSLMLQEGPFLSEIENIRKPHLEFDYLRHIOFHTROPQGYGNDSENYM 368
QY 360 SGNVSTPSPISGNDITSPFYGKSEPVONLEFNGEKYRAVANINLAWPASA-VYSG 418
DB 369 SGNVSTPSPISGNDITSPFYGKSEPVONLEFNGEKYRAVANINLAWPASA-VYSG 428
QY 419 VTKVEFSQYNDQDEASTQYDYSKRNVAAS-NDSDIDQLPETTDEPLEGYSHQNLNYM 477
DB 429 VTKVEFSQYNDQDEASTQYDYSKRNVAAS-NDSDIDQLPETTDEPLEGYSHQNLNYM 488
QY 478 CFLMDSRGRTIPVLTWTHKSVDFPNMDSKRTIQLPVKAYKLSQASVAVAGPRTGDI 537
DB 489 CFLMDSRGRTIPVLTWTHKSVDFPNMDSKRTIQLPVKAYKLSQASVAVAGPRTGDI 548
QY 538 IQCTE-NGSAAITIVT-PDVSYSQKRYARIRHIVASTQITFTLSLDGAPNOYFDTINK 595
DB 549 LFLKSSNSIAKPKRYLNSAALLQRYRVRIRASTTNLEFVONSNDLVIYINKTMK 608
QY 596 GDTLTYSFNLASFSTPELGS--NNLQIGVTGLSAGDKVYIDKIEFIV 643
DB 609 DGDLTGTFTPATNSNMFGSGDNDIIGAESFVNEKIYIDKIEFIV 658

RESULT 5
ID C8AA_BACUR STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin
DE CryVIIIa) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN CRY8AA OR CRYVIII(A).
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RX NCBI_Taxid-132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NRRL B-18746 / PS50C;
RA Payne J.M., Sick A.J., Fonceirada L.;
RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
RT gene encoding a coleopteran-active toxin."
RL Patent number EP0498537, 12-AUG-1992.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

```

SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.

CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC EMBL: U04364; AAA21117.1; -

DR HSSP: P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

DR Toxin: Sporulation.

SO SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;

Query Match 36.4%; Score 1240; DB 1; Length 1157;
Best Local Similarity 40.2%; Pred. No. 8.7e-74;
Matches 275; Conservative 116; Mismatches 231; Indels 62; Gaps 17;

1 MNPNNREHDTIKTENNEVPTNHVOYPLAETPNPTLEDINREKFLMTADNTEALDSS 60
1 MSPNNONEYEIIDATPTSTVSSDSNRKPFANEPDANNNYDYLMKSGENPELEGFP 60

61 TT---KDVIOKGISVVDLLGVGFPFGALVSEYTNFLNTIMPSE--DPMKAFMEYEA 115
61 ETFFSSSTIGTIGIYRIIGALGVPPASQIASFPIVQOLMPSKSDVIMGEIMEVEE 120

116 LMDDKINDYAKKNAELAGLONNVEDYVSAISSMOKNPSSRNPHSGRIELESQAE 175
121 LVQDKIEKYKDALBELKIGNALDYQOSLEDMENRDAR---TRVSYNQFIIDL 177

176 HFRNSMPSFALSGEYVLEFVYVQAANTHLFLKDAQIYGEEMGYEKEDIAEFKROLK 235
178 NFVSSIPSFASVGHVLLAVYAOAVMLHLRLDASIFGHEMGFTGGEISRFYNROVOL 237

236 TOEETHDCVKNYVNGDLKRGSSSESWNFRNRYREMTLVLDLALFPLYDVLYPKY 295
238 TAEVSDVCVKNYKIGDLKGTSTKSMNLHOFREMTLVLDVLYALFPYDTHMYPIET 297

296 KTELRLVLTDPYV-GVNNLGRY-----GTFFSNIE-NYIRKPHLEFYLRIQFHR 345
298 TAOITROVYTPPIAFNIVTSTGFCNPMSTHSGILFEVENNVIRPHFLDILSSVEINTS 357

346 FQPGYVGNDSF-NWSGMNVSTPDSIGSNDITTSPPFGNKSSE-----P 388
358 RGGITLNDAYINWSGHTLTKYRRRTADSTVYTAN-YGRITSEKNSFALDREDIIEINST 416

389 VONLEFNKEKYRAVANNNLAVMPASVAGYTKVEFSOYNQTD--EASTQYTSKRWVG 446
417 VANLANIYQKAGVPGS-----WFMVAKRGSTTAYITXTHALQOCCTVYESS----- 467

447 AVSMDSIDQLPETDEPLEKGYSHQNLVYM--CELMQGR--GTIPVLTTHRSVDEFN 502
468 -----DEPLDRT-VVAESYSHRLSHITSHSPKNGASAYGSPFVFWTHHSADINN 519

503 MIDSKKTIQPLVYKAYKQASQASVYAGPRFGGDIIOCTENGSAATIVTDDVYSOKYR 562
530 TYSKTIQIPIAVKDMKLYLGSGVVGPGFGDILKTKTNSIIGTFNAVYNGSLQKR 579

563 ARIHASTQSITFTSLDGAPENOYFPDKTINKGDTILTYNSFNLASFSTPEEL--SGNUL 620
580 VAIKRASTIDREFETLVL-GDTIEKNRPFKTMONGASLVEYEFKFASTIDFQFRETQKI 638

621 QIGVTLGSLAGRVYIDKIEFIPVN 644
639 LTSMGDFSSSGDEVYIDRIEFIPVD 662

RESULT 6

CCB8A_BACUR STANDARD; PRT; 1169 AA.

ID C8BA_BACUR 045705;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry8Ba (insecticidal delta-endotoxin

DE CryIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa crystal

DE protein)

GN CRY8BA OR CRYIIIB(a) OR 50C(B).

OS Bacillus thuringiensis (subsp. kumamotoensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_Taxid=132267;

RN [1]

RP STRAIN=NRRL B-18746 / B550C;

RA Michaels T.E., Fencerrada U., Narva K.E.;

RT "Process for controlling scarab pests with Bacillus thuringiensis

RT isolates."

RL Patent number WO9315206, 05-AUG-1993.

CC - FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABEID BEETLES.

CC - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC EMBL: U04365; AAA21118.1; -

DR HSSP: P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

DR Toxin: Sporulation.

SO SEQUENCE 1169 AA; 133543 MW; 22EECF5BD699909 CRC64;

Query Match 34.9%; Score 1187; DB 1; Length 1169;
Best Local Similarity 38.8%; Pred. No. 2.7e-70;
Matches 260; Conservative 141; Mismatches 231; Indels 38; Gaps 22;

1 MNPNNREHDTIKTENNEVPTNHVOYPLAETPNPTLEDINREKFLMTADNTEALDSS 60
1 MSPNNONEYEIIDATPTSTVSSDSNRKPFANEPDANNNYDYLMKSGVSEIPGSP 60

61 -----TTKDVIOKGISVVDLLGVGFPFGALVSEYTNFLNTIMPSE--EDPMKAFMEYEA 114
61 EVFLSEGDVAKAALDIYKGLTIGGVFPVPIYSLYQLDILMPSKQKQMEIFMEYOE 120

115 ALMDQKADYAKKNAELAGLONNVEDYVSAISSMOKNPSSRNPHSGRIELESQAE 174
121 ELINOKIAEYARNAKALSELGLGNNVQLYTLAEEMENENGRS--ALDVRNREIIDL 177

175 SHFRNSMPSFALSGEYVLEFVYVQAANTHLFLKDAQIYGEEMGYEKEDIAEFKROLK 234
178 SLFQYMPSEFVYTFEYEPFLTYMANNLHLRLDASIFGHEMGFTGGEISRFYNROVOL 237

235 LTOEETHDCVKNYVNGDLKRGSSSESWNFRNRYREMTLVLDLALFPLYDVLYPKY 294
238 LTAESDVCVKNYKIGDLKGTSTKSMNLHOFREMTLVLDVLYALFPYDTHMYPIET 297

296 KTELRLVLTDPYV-GVNNLGRY-----GTFFSNIE-NYIRKPHLEFYLRIQFHR 348
298 TTAQITREYVYDPLGADVDPNIGSMYKADSESELEKAAIRPFAVDYITGLVYTK-KR 356

QY 349 GYGNDSFNWGSNVSTRPSIGSNDITSPFYGNKSSSEPVONLEFNGEKYRAVANTLU 408
 Db 357 SFTSDRYMRWAGHQISYK-HIGTSSTFQMYGTQNLQSTSNFPTNNDIYKITSNGAV 415
 QY 409 ---AVMPSAVYS--GVYKVEFQYNDQTDASVQYI-DKRNVAWSIDQLPPTTD 462
 Db 416 LLDIVYGYTYTTPGMEFEFVNLNTRKLTLYKPAKSDIIDTRTSELELPPETSG 475
 QY 463 EPLEKGYSHOLNYMCFMLOGSNGT-IPVLTWTKSVDFEPMNDISKITQLVYAVYKLO 521
 Db 476 QPNVESYSHRLGHI-FTIVSSSTSTVYVPSMHRASADLTNTYKSGEITQLGKGSSTTG 534
 QY 522 SGASVYAGPRFTGCDIIQCTEN-GSAATYVTPDVYSOKYRARIHYAS--TSQIT-FTL 577
 Db 535 RNTYIKGRGYTGGLVALTRDGRSCFQIMFPE--SQRFRIIRYASNETSYSLYGL 591
 QY 578 SLUGA-PFNQYFEDKTIKNGDFTLYNSFNLASSTPPEL-SGNNOIGVYGLSAGDKYI 635
 Db 592 NQSGTLKFNQYTSNK--NEND-LTYNDFKTYEIPRIVISYVASSNTQRLSIGQNTNLF 648
 QY 636 -DKIEFTPVN 644
 Db 649 LDRIEFIPVD 658

RESULT 7

CLIB_BACTE STANDARD: PRT: 719 AA.
 AC 045709;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
 CryII(b) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 GN CRYIIB OR CRYIIB(b) OR CRYV OR CRYV465.
 OS Bacillus thuringiensis (subsp. entomocidus).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1436;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BP465;
 RX MEDLINE=95314293; PubMed=7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.I.;
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus
 thuringiensis and cloning of cryV-type genes from Bacillus
 thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
 entomocidus." Microbiol. 61:2402-2407(1995).

CC Appr. Envitron. Microbiol. 61:2402-2407(1995).
 CC EPIHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC ACTIVE ON PLUTELLA XYLOSTELLA BUT NOT ON BOMBYX MORI.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY

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CC EMBL: U07642; AAA82114.1; --

DR HSP: P02965; ICY.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SO SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;

Query Match 34.6%; Score 1178; DB 1; Length 719;
 Best Local Similarity 38.6%; Pred. No. 5,3e-70;
 Matches 256; Conservative 132; Mismatches 234; Indels 42; Gaps 15;

QY 1 MNPNNRSEHDTYKTTEN-NEVPNNHYOYPLAETPNT---LEDLVYKEFLKRTADNNTGA 56
 Db 1 MKLKNPKKHOSLSNAKVDKIATDSLK-----NETDIELKNNMNEYLRN--SEHS 50
 QY 57 LBSSTTKDVIQKISVYGDLLGVVGFPGALVSTFNEFLNTP-SDPMKAFMEQVEA 115
 Db 51 IDPFVSASTIQTIGIAGKILGTLGVFAGQGLASLYSFLIGLTKMGKSGMEIFENHVEE 110
 QY 116 LMDQIADYAKNKALELDGLONNVNDVYSAISSQKNKPNVSRNPHSGRIRELSQAES 175
 Db 111 IINQKILITTRAKNALSGLDGLDALVYHESLESWEV---RNNTRARSVYKNOYIALEL 167
 QY 176 HFRNSMPSFASISGEVLEFTTYAQAANTHLFLKDAQOYGEEMGEKEDIAEFYKROLK 235
 Db 168 MFYQKLPFAVSEGEVPLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNROVER 227
 QY 236 TOEYTHCYKATNVGLDKLRGSSYSWVNFNRYREMTLVLDLALFPLVRLYREV 295
 Db 228 TRDYSDHCIKWNTGTLNLRGTNAKSWRYNQFRDMTLAVLDLVALEPPSYDLYPIKT 287
 QY 296 KTELFRDVLTDPIVGVNNGYGT-----PSNIE-NYIKRPHLPDLRIQPH-- 343
 Db 288 TSQITREYVTDALIGYHPQAFASTTWTNNNAPSFALEAAVIPSPLDLFLEKVTYSL 347
 QY 344 -TRFOPGYGNDSPFVWGSNVSTRPSIGSNDITSPFYGNKSSSEPVONLEFNGEKYRA 402
 Db 348 LSWMSNTQY---MMWGGHRLSRPRIGALNTSFG-STWTSINP-TIQFTSRDYRT 401
 QY 403 VANTNLAVPASAIVSGYKVEFQYNDQTDASVQYI-DKRNVAWSIDQLPPTTD 461
 Db 402 ESTAGLNLFLTPVGVNPRVDHMKFPPLPIASDNFYLLGAVAGTQLOOSENLPEPTT 461
 QY 462 DEPLEKGYSHOLNYMCFMLOGSNGTIPVLTWTKSVDFEPMNDISKITQLVYAVYKLO 521
 Db 462 GQPNVESYSHRLSHI--GLISASHYKALVYSWIRASDRNTIPNSITPIPLKKNLS 519
 QY 522 SGASVYAGPRFTGCDIIQCTENGSAATYVTPDVYSOKYRARIHYASTSQITFTSLDG 581
 Db 520 SCAAAVVRPFGFGDILIRNTGTGDIRVNIINPFAQRYRVRIRYASTDLOFHNSING 579
 QY 582 AFNQYFEDKTIKNGDFTLYNSFNLASSTPPELSS--NNLOIGVYGLSAGDKYIDKIE 639
 Db 580 KAINQGNFSATMNGEDLDYKTFRTIGFTTFPSFSDVQSTFTIGAMNFSGNEVYIDRIE 639
 QY 640 FIVP 643
 Db 640 FIVP 643

RESULT 8

CLIB_BACTE STANDARD: PRT: 719 AA.
 AC 09XDL1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
 CryII(b) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 GN CRYIIB OR CRYIIB(b) OR NRCRYV.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1426;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BR30;
 RX MEDLINE=20374042; PubMed=10919402;
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein

RT gene.;

CC Curr. Microbiol. 41:65-69(2000).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE. ACTIVE ON PLUTELLA

CC XYLOSTELLA AND ON BOMBYX MORI.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC or send an email to license@isb-sdb.ch).

CC

DR EMBL: AF047579; AAD44366.1; -

DR HSP: P02965; 1C1Y

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00355; endotoxin; 1.

DR Toxin: Sporulation.

DR KW

DR SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 34.5%; Score 1176.5; DB 1; Length 719;

Best Local Similarity 40.4%; Pred. No. 6,7e-70;

Matches 236; Conservative 114; Mismatches 232; Indels 31; Gaps 12;

28 PLAEPTLEEDLYKFEKRLMTADNTEALDSTTKDVIKGISVVDLGVGFPFGA 87

DB 25 PLEHNTMELONSHEEDOLCKEVESEPEVSVST--IGTGIGACKIGLGNLCPAGQ 81

QY 88 LVSTYTNPLNTIP-SEDPKAFMEQVEALMDQRIADYAKNAELGLONNEDVYSA 146

DB 82 VASLYSTFLGLWPKGSKQWEIEMEHEBELNOKISTYARKKALADKGLADLANVHES 141

QY 147 LSSQKPNVSSRNPHSGRIARELSQAESHRNPSFAISGVLEFLTYAQAANTHLEF 206

DB 142 LESHTEN---KNTNRVSVYVANOIATLELMVQKLPSPVSGEEVPLPIYAQAANTHLL 198

QY 207 LKDAQIYGEEMGYEKEDIAEFYRQKLTQOYTDHCYKYNVGLDKRGSYSQWTFN 266

DB 199 LLRDAISFGKEMGLSESEISFYNNROSSQOQYEDYDCEMYNTGLNRLGTNAESWVRN 258

QY 267 KYRREMTLVLDLALPFLYDVRLYPKKEVKELRDVLTDPVGNVNLRGGT----- 320

DB 259 QFRDMTLMVLDLVALFESYDTRMTPIPTSAQLTREVYTDALGIVHPNASTTWTNNN 318

QY 321 ---SNIE-NYIRKPHLFYDLHRIQFH---TRQPGYVYGNDSFYWGSVYSTRPSISGN 373

DB 319 APSFTIDAAVVRNHLDFLEQYTIYSLSRMSWTFY---MMNMGCHKLEFR-TIGGT 373

QY 374 DIISPFYGNKSSPEYQVLENGEYVYRAVANTLAMPASVAGTYVEES-QYNQDQD 432

DB 374 LNTSTQSTNTSINPV-TLPFTSRDYVFTESLAGLNTLTPVNGVPRVDMFHMVHPHPI 432

QY 433 EASTQYSGKRVGAVSWDSIDQLPPTDEPLEKGYSHQNVYVCFMQSGRGTPIYLT 492

DB 433 ASDNYYGYAGIGTQDQDSENEPPTTGGPNTSYSHRSLH--GLISASHVALYVS 490

QY 493 WTKASVDFNMIDSKRITQPLVYKAYKLOSGASVAVGFRFTGGDIIQCTENGSAATYVT 552

DB 491 WTHRSADRTNTINSITQIPLVYKAFNLPJSGASVAVGFRFTGGDIIQCTENGSDIVYN 550

QY 553 PDVYSQKRAIRIHASVQITFTSLDGAFFNQYFDKTIKGGTLTYNSNLAISFSTP 612

DB 551 INPPAQQRRLIRIRYASTTNEEHTSINKALINQNSFATMNRGDDLDKARIVYGTTP 610

QY 613 FELSG---NNLQIGVYGLSAGDKVYIDKIEFIV 643

DB 611 FFSNAGSTFTTIGANNFSLNGNEVYIDRIEYFV 643

RESULT 9

CC C7AB_BACUK STANDARD; PRT: 1138 AA.

AC 045708;

DR 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DR 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry7ab (insecticidal delta-endotoxin

DE cry7ab(b) (crystalline entomocidal protoxin) (130 kDa crystal

DE protein).

GN CRY7AB OR CRYVIA(B).

OS Bacillus thuringiensis (subsp. kumamotoensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=133267;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HD867;

RA Payne J.M., Fu J.M.;

RT Coleopteran-active toxins.*;

RT coleopteran-active toxins.*;

RL Patent number US5286486, 15-FEB-1994.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF COLEOPTERA.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC

DR EMBL: U04368; AAA21121.1; -

DR HSP: P07130; 1DLG.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00355; endotoxin; 1.

DR Toxin: Sporulation.

DR KW

DR SEQUENCE 1138 AA; 129658 MW; E12DC80C0A56DIDA CRC64;

Query Match 34.5%; Score 1174.5; DB 1; Length 1138;

Best Local Similarity 38.3%; Pred. No. 1.7e-69;

Matches 236; Conservative 114; Mismatches 235; Indels 67; Gaps 18;

QY 1 MNPNRSEHDTITTENEVPTNHYQPIAETNPTELENYKELMTADNTEALDSS 60

DB 1 MNLNLTGGE-----DSNRLNNSLNPTQKALSPKNNYODFLITERQPEALAG 55

QY 61 TTKVDYKIGSVYVDLGVGFPFGCALVSFYTNFLNTIP-SEDPKAFMEQVEALMDQ 119

DB 56 NT-AINTVAVSYGATISALGVPGASFTTNFYKLTGLMPHDKNTMDEFTVEVLEID 113

QY 120 KIADYARKKALAELOGQNNVEDYVSAISSQKPNVSSRNPHSGRIARELSQAESHRN 179

DB 114 KIRQYARKKALAELEGNNLTIIYQALQEDMLNPP---DDPATTVYIDRFLDALFES 170

QY 180 SMPSPAISGEVLEFLTYAQAANTHFLDLDAQIYGEEMGYEKEDIAEFYRQKLTQOY 239

DB 171 YMPSEFRVAGEIPLITYAQAANTHLLDLRSTLYGKMEFTQNNLENNRQKHLISEY 230

QY 240 TDHCVKMYNVGLDKRGSYSVYVNRNRYRREMTLVLDLALPFLYDVRLYPREVETL 299

DB 231 SNHCYKWTNSGLSTRNGSTIYQWNTNFRREMTLVLDLAAVFPYIDPDMYSHSTOL 290

QY 300 TRDVLTDPI-VGVNNLRGYGTTFNSIEN-YIRKPHLFYDLHRIQFH-----RFQPG 349

```

Db 291 TREYVTPDISLISN-DGIPSPSOMENTAIRTPHLVDYDELYTSKKAESHEIQP 349
Qy 350 YGNDSPFNWNGVSTRPSIGSNDITSPYGNKSEPVON--LEFNGEKYRAVANTN 407
Db 350 LF-----YSAHVSPKSEQSN-LTTGTIGY-KTSGYISSGAVSRGDIYRTLAAPS 401
Qy 408 LAVPMSAVSGVTKVEFSQYNDQDEASTQYDSKRNVAVSWSIDQLPETTDEPLEK 467
Db 402 VVVVPPYQNVGEQVEFEYGVKGVHVRGDKYD-----LTVDSIDQLPPD--GEPIHE 452
Qy 468 GYSHOLNVYVCFLMG--SRGITPVLTWTHKSVDFPNMIDSKITQLPLVAKYKLSGA 524
Db 453 KTHRLCHATAISKSTPDYDNATIPFSWTHRSAEYNNRIYPNKIKIPAVKMYKLGDS 512
Qy 525 SVVAGPRTGGDIIOCTENGSAATVYTPDVYSQKRAIRIHYASTQSITFLSLDGAFF 584
Db 513 TVKGGPFTGDLVKRSGNIGIDIKATVNSPLSQYRVARVRAIVN-----SGQF 563
Qy 585 NOYFEDK-----TINKGDTLYNSFNLASFSPFELSGNN--LOIGVGLSAG 630
Db 564 NVYNKDKITLQRRKQWVTEIGEGKDLTGSGFYETSTTIQPPDKHPKITLHLSDLNN 623
Qy 631 DKYIDKIEPIPN 644
Db 624 SSFYVDSIEPIVD 637

RESULT 10
C7AB_BACUA STANDARD: PRT: 1138 AA.
AC 045707:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cry7Ab (insecticidal delta-endotoxin
DE protein)(b) (crystalline entomocidal protoxin) (130 kDa crystal
GN CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HD511:
RT Payne J.M., Fu J.M.:
RT "Coleopteran-active toxins";
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPROUTATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL: U04367; AAA21120.1; -.
CC HSSP: P07130; 1DLC.
CC InterPro: IPR001178; Endotoxin.
CC Pfam: PF00555; endotoxin; 1.
CC Toxin: Sporulation.
CC SEQUENCE 1138 AA; 129778 MW; 01DF072C074CE88 CRC64;

```

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Query Match 34.0%; Score 1159.5; DB 1; Length 1138;
Best Local Similarity 38.2%; Pred. No. 1,7e-68;
Matches 254; Conservative 119; Mismatches 243; Indels 49; Gaps 17;

Qy 1 MNPNNSEDDTJKTENNEVPNNHVOYPLAETPNPLDLNKEFLRMTAANNFALDSS 60
Db 1 MNLNLGVE-----DSNLTNLSLNTPTQKALSLKLNMYODLTSTEEDEQEPALASG 55
Qy 61 TTKDVIQKISVYDGLGVGPPFGGALVSEYTNFLNTMP--SEDPKAFMEQVEALMDQ 119
Db 56 NT--AINTVSVTGTALALGVGASFTTNFLYKLTGGLMHPNNKINIMDEFMTVEETLEQ 113
Qy 120 KIADYAKNKALAELOGLONNVEDYVSALSQKPNVSSRNHSGRITELDSQESHPRN 179
Db 114 KIEQYARKKALAELEGLNNTLITYOQLEDMNPN--DDPATYTRVDRRLDALAES 170
Qy 180 SMPFAISGEYELFLTTYAOAANTHLFLKDAQIYGEEMGEKEDIAEFYRQLKQY 239
Db 171 YMPSEFVAGYEIPLTLVYAQAANLHLALRDLSTLGDKNFTQNNIENYRQKKHISEY 230
Qy 240 TDCYKWTNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTEL 299
Db 231 SNHCYKWTNVGLSRGSLNGSTYEQMINYRFRREMLLVLDIAVPPIDPRMYSMETSQOL 290
Qy 300 TRDVLTPDI-VGVNNLRGVTGTFESNIEN-YLRKPHLDYLRIOFPH-----RQPG 349
Db 291 TREYVTPDISLISN-DGIPSPSOMENTAIRTPHLVDYDELYTSKKAESHEIQP 349
Qy 350 YGNDSPFNWNGVSTRPSIGSNDITSPYGNKSEPVON--LEFNGEKYRAVANTN 407
Db 350 LF-----YMCVHKVSEFKSSQSN-LYTTGIGY-KTSGYISSGAVSRGNDIYRTLAAPS 401
Qy 408 LAVPMSAVSGVTKVEFSQYNDQDEASTQYDSKRNVAVSWSIDQLPETTDEPLEK 467
Db 402 VVVVPPYQNVGEQVEFEYGVKGVHVRGDKYD-----LTVDSIDQLPPD--GEPIHE 452
Qy 468 GYSHOLNVYVCFLMG--SRGITPVLTWTHKSVDFPNMIDSKITQLPLVAKYKLSGA 524
Db 453 KTHRLCHATAISKSTPDYDNATIPFSWTHRSAEYNNRIYPNKIKIPAVKMYKLGDS 512
Qy 525 SVVAGPRTGGDIIOCTENGSAATVYTPDVYSQKRAIRIHYASTQSITFLSLDGAFF 584
Db 513 TVKGGPFTGDLVKRSGNIGIDIKATVNSPLSQYRVARVRAIVN-----SGQF 563
Qy 585 NOYFEDK-----TINKGDTLYNSFNLASFSPFELSGNN--LOIGVGLSAG 630
Db 564 NVYNKDKITLQRRKQWVTEIGEGKDLTGSGFYETSTTIQPPDKHPKITLHLSDLNN 623
Qy 631 DKYIDKIEPIPN 644
Db 624 SSFYVDSIEPIVD 637

RESULT 11
C1BB_BACTU STANDARD: PRT: 1229 AA.
AC 045739:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
DE protein)(b) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN CRYIIB OR CRYIB(B) OR CRYETS.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BG5847 / NRRL B-21110;
RC Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.:
RT "Bacillus thuringiensis cryeIa and cryeIb toxin genes and proteins
RT toxic to lepidopteran insects";
RL Patent number US5322687, 21-JUN-1994.

```

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC
 CC EMBL: L32020; AAA22344.1; -
 CC HSSP: P02965; ICIT.
 CC InterPro: IPR001178; Endotoxin.
 CC Pfam: PF00555; endotoxin; 1.
 CC Toxin: Sporulation.
 CC KW SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
 SQ
 Query Match 34.0%; Score 1156.5; DB 1; Length 1229;
 Best Local Similarity 37.9%; Pred. No. 3e-68;
 Matches 250; Conservative 117; Mismatches 254; Indels 39; Gaps 14;
 QY 1 MNPNNSEHDITKTENNEVPTNHVQPLAETPNPLE---DLNKEFLMRTADNTEAL 57
 DB 1 MTSNRKNEHEIT-----NALSTPVSNPSTQNLSPDARIIDSLCVAEWNIDPF 50
 QY 58 DSSTKDVIOGIGSVYDGLGVGPPGALVSYFTNFLTNPIS-EDPKARMEQVEAL 116
 DB 51 VSAST---VQGINIAGRIIGLVGVPAGOLASFTVLGELMPSGRDPWEIYLEHEDL 107
 QY 117 MDQIADYAKKNAELQGLONNVEDYVALSSMOKNPVSSRNPHSGRIRLEPSQAESH 176
 DB 108 IRQOYTEMTRNTAIFARLEGGRYSYQALLETWLDNRNDAR---SRSLIERVVALELD 164
 QY 177 FRNSMPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEXEKDIAEFKROKLT 236
 DB 165 ITTALPLFRINNEEVPPLMVAQAANHLHLRLDASLGSEMGMASSDVQVIOEORIT 224
 QY 237 OEYTDHCYKYNVAVGLDKRGSSYEWNFNRYRREMTLVLDLALFPLVDVRLYPREK 296
 DB 225 EYSNHCQVWNTGILNLRGTNAESWLRYNQFRDLTLGLVDLALFPPSYDTRYPINTS 284
 QY 297 TELTRDVLTPDIVGVNUNLRGYGT-----FSNIENYI-KRPHLFDVLRHQFTFR 346
 DB 285 AQLTREITVDIGRTNAPSFGASTNMFNNNAPSFALEAIFRPHLDEPEOULTISA- 343
 QY 347 QPGYVNDSPFVNSGNYSTRPSIGSNDILTSFPGKSSPEVONLEFNGEKYRAVANT 406
 DB 344 SSRWSTQHMNTWVGHRLNFRPIGTLNTSIOGLTNNISNPV-TLOFTSDVYRTESNA 402
 QY 407 NLAVPSAVYSGVTKVEFSQYNDOT-DEASTQYTDK-RNVAVNSQSIDLPETIDEP 464
 DB 403 GTNILEFTPVNGVFWARBNFINPONIERGATYISOPVQVGIOLFDESELEPETERP 462
 QY 465 LEKQSHOLNVMCFLMGSGNGTIPVLFWTHKSVDFEMIDSKITDLPVAKAKLOSGA 524
 DB 463 NYESSHRSLSH--GLIIGNTLRADVYSWTHSADRTWTIGPNKTIQPLKALNLSGV 520
 QY 525 SYVAPREFTGDIIOCTENGSAATYTVPDVYSOKYBARIHVASTOITFTLLSDGAPF 584
 DB 521 TVVGSGCFTGDIILRTMGTGFDIRLNIINVPLOSRYRVRIRVASTDLOFRTITV 580
 QY 585 NQYEDKTIKGDITLYSFNLAISTPEL--SGNNQIGVTLGASGDYKDYIDKIEIP 642
 DB 581 NIGNSERTMNRDNLERSFRTAGSTPEPNFLNASTFTLLGAQSF--NQEYIDRVERVP 639

RESULT 12
 CIBC_BACTM STANDARD; PRT: 1233 AA.
 ID CIBC_BACTM
 AC 045774;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIbC (insecticidal delta-endotoxin
 DE CRYIbC(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN CRYIbC OR CRYIbC(c) OR CRYIbC.
 OS Bacillus thuringiensis (subsp. morrisoni).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1441;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bishop A.H., Bone E.J., Ellar D.J.;
 RT Cloning of novel Bacillus thuringiensis delta-endotoxin.";
 RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC
 CC EMBL: Z46442; CA86568.1; -
 CC HSSP: P02965; ICIT.
 CC InterPro: IPR001178; Endotoxin.
 CC Pfam: PF00555; endotoxin; 1.
 CC Toxin: Sporulation.
 CC KW SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
 SQ
 Query Match 34.0%; Score 1156.5; DB 1; Length 1233;
 Best Local Similarity 37.9%; Pred. No. 3e-68;
 Matches 250; Conservative 117; Mismatches 254; Indels 39; Gaps 14;
 QY 1 MNPNNSEHDITKTENNEVPTNHVQPLAETPNPLE---DLNKEFLMRTADNTEAL 57
 DB 1 MTSNRKNEHEIT-----NALSTPVSNPSTQNLSPDARIIDSLCVAEWNIDPF 50
 QY 58 DSSTKDVIOGIGSVYDGLGVGPPGALVSYFTNFLTNPIS-EDPKARMEQVEAL 116
 DB 51 VSAST---VQGINIAGRIIGLVGVPAGOLASFTVLGELMPSGRDPWEIYLEHEDL 107
 QY 117 MDQIADYAKKNAELQGLONNVEDYVALSSMOKNPVSSRNPHSGRIRLEPSQAESH 176
 DB 108 IRQOYTEMTRNTAIFARLEGGRYSYQALLETWLDNRNDAR---SRSLIERVVALELD 164
 QY 177 FRNSMPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEXEKDIAEFKROKLT 236
 DB 165 ITTALPLFRINNEEVPPLMVAQAANHLHLRLDASLGSEMGMASSDVQVIOEORIT 224
 QY 237 OEYTDHCYKYNVAVGLDKRGSSYEWNFNRYRREMTLVLDLALFPLVDVRLYPREK 296
 DB 225 EYSNHCQVWNTGILNLRGTNAESWLRYNQFRDLTLGLVDLALFPPSYDTRYPINTS 284
 QY 297 TELTRDVLTPDIVGVNUNLRGYGT-----FSNIENYI-KRPHLFDVLRHQFTFR 346
 DB 285 AQLTREITVDIGRTNAPSFGASTNMFNNNAPSFALEAIFRPHLDEPEOULTISA- 343
 QY 347 QPGYVNDSPFVNSGNYSTRPSIGSNDILTSFPGKSSPEVONLEFNGEKYRAVANT 406
 DB 344 SSRWSTQHMNTWVGHRLNFRPIGTLNTSIOGLTNNISNPV-TLOFTSDVYRTESNA 402

QY 407 NLAVPMSAVSYGVTKVEFSQYNDOT--DEASTQFYDSK--RNVGAVSMDSIDOLPPEITDDEP 464
 Db 403 GTNILEFTPVNGVPMARFNINQONITKERTATISPOYGVGIGLFDSETELEPETERP 462
 QY 465 LEKYSIQLNVMWCMFLMOGSRGTIPVLWTNHSKVDFPNMIDSKKITQPLVAVAKLOSGA 524
 Db 463 NYESYSHRLSHI--GLTIGTTLRAPPYSWTHRSADRTNIGPRLTQIPLVAKMLNHSGV 520
 QY 525 SVVAGPRTGDIIOCTENGSAATYVTPVPSYOKRYRRIHAYASTQTFLLSDGAF 584
 Db 521 TVVGGPEFTGDIILRNNTCTFEDIRLNINVLPSQNTKRVIRINASTTDLQFTFRINGTIV 580
 QY 585 NQYFEDTKIKGDTLYVNSFNLASFSSTPEL--SGNNLQIGYGLSAGDKVYIDKIEFIP 642
 Db 581 NIGNSFTNMRGNLERSFRAGFSTPFNFMAQSTFLGASPS--NQEYIDVNEVEVP 639

RESULT 13

CITA_BACTK

ID CITA_BACTK STANDARD; PRT; 719 AA.

AC Q45752; Q45750; Q45751; Q45756; P71092;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cyIIa (insecticidal delta-endotoxin
 DE CryII(a)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 GN CRYIIA OR CRYII(A) OR CRYV OR CRYVI OR CGCRYV.
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_Taxid=29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D51R732;
 RX MEDLINE-93298009; Pubmed-8517758;
 RA Gleeve A.P., Williams R., Hedges R.J.;
 RT Screening by polymerase chain reaction of Bacillus thuringiensis
 RT serotypes for the presence of cryv-like insecticidal protein genes and
 RT characterization of a cryv gene cloned from B. thuringiensis subsp.
 RT kurstaki.";
 RL Appl. Environ. Microbiol. 59:1683-1687(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JHCC4835;
 RX MEDLINE-92269582; Pubmed-1588820;
 RA Tallor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
 RT Identification and characterization of a novel Bacillus thuringiensis
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
 RL Mol. Microbiol. 6:1211-1217(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HD-1;
 RX MEDLINE-95314293; Pubmed-7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
 RT Distribution of cryv-type insecticidal protein genes in Bacillus
 RT thuringiensis and cloning of cryv-type genes from Bacillus
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
 RT entomocidus.";
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AB88;
 RX MEDLINE-96178985; Pubmed-8606196;
 RA Kostelchka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
 RA Craig J.A., Kozel M.G., Estruch J.J.;
 RT Cloning of a cryv-type insecticidal protein gene from Bacillus
 RT thuringiensis: the cryv-encoded protein is expressed early in
 RT stationary phase.";
 RL J. Bacteriol. 178:2141-2144(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-61;
 RA Selvapandian A., Bhatnagar R.K.;

RT "Isolation, cloning and expression of cryv gene.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC ACTIVE ON PLUTELLA XYLOSTELLA AND BOMBYX MORI.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENOTOXIN FAMILY.
 CC
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DR EMBL: M86544; AAA22354.1; -
 DR EMBL: X62821; CAA44633.1; -
 DR EMBL: I36338; AAC36999.1; -
 DR EMBL: I49391; AAB00958.1; -
 DR EMBL: Y08920; CAA70124.1; -
 DR HSSP: P02965; ICTY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 KW Toxin; Sporulation.
 FT VARIANT 159 159 K -> R (IN STRAIN 61).
 FT VARIANT 233 233 D -> Y (IN STRAIN JHCC4835 AND HD-1).
 FT VARIANT 443 443 A -> V (IN STRAIN AB88).
 FT VARIANT 711 712 KO -> NE (IN STRAIN HD-1 AND 61).
 SQ SEQUENCE 719 AA; 81216 MW; 3627E9AC25DAF5 CRC64;

Query Match 33.9%; Score 1156; DB 1; Length 719;
 Best Local Similarity 38.0%; Pred. No. 1.5e-68;
 Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

QY 1 MNPNRSEHDITKTEN--NEVPTNVOYPLAETNPT---LEDNLYKEFLMADNNTA 56
 Db 1 MLKMDKHOSFSSNAKYDKISTDSLK-----NETDIELQNNHEDCKMSKEYEVEP 53
 QY 57 LDSSTTKVDYONGISVVDLLGVVGFPGALVFFYNFLMTWP--SEDMKAFMEQVYA 115
 Db 54 FVSAST---IQGIGIACKIIGTIGVPPAGVAYALYIFIGELMPKKNMETFMEEVIE 110
 QY 116 LMDQKIADYAKNKALAEQGLQNNVEDYVSLSSWQKNPVSSRNPHSQGRIRLFQOAS 175
 Db 111 IINOKISTYARKKALTDLKGLDALAVYHDSLESWGN---RNNTARSVYKQYIALEL 167
 QY 176 HERNMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYEEGKEDEDAEYKQQL 235
 Db 168 MEYQKLPFAVSGEVEPLLPITYAQAANLHLLDASIFKEGELSSSEISTFYNQOVER 227
 QY 236 TOEYDHCYKRYNVGLDKLGSSYESVWNNFRRYRREMTLVLDLIALFLPYDRLPKFY 295
 Db 228 AGDYSDDHCYKRYSTGLNKTNAESWVRYNPFQDMTLVLDLVALFSDYDQMPIT 287
 QY 296 KTELRLDVLTPDIYGVNNLNGYGT-----FSNIE-NIRKRLHLDYLRHQFH-- 343
 Db 288 TQOLTRFYDAITGVPHPSFTSTWYNNAPSFSAIEAAVRNPHLDLFEQVYISL 347
 QY 344 -TRQPGYGGNDSFNWYSGVSTRPSISNDITTFPGNKSSEPVQNLKENGKGVYA 402
 Db 348 LSRMSNQY---NMNMGGHKLERR-TIGTLMISTOGSNTSINPV-TLPFTSRDYVT 401
 QY 403 VANTNLAWVPSAYSGVTKVEFS-QYNDQDEASTQTYDSKRNVGAVSMDSIDOLPPEIT 461
 Db 402 ESIAGLNLFLTOPVNGVRVDFMKFVTHPIASDNFYYPGAVIGIQGLDSDSNELPEAT 461
 QY 462 DEPLEKGYSHQNLVWCMFLMOGSRGTIPVLWTNHSKVDFPNMIDSKKITQPLVAVAKLO 521

DB 462 GPNYESYSHRLSHI--GLISASHVKALVSWTHRSADRTNTEPNSITQIPLVKAPNLS 519

QY 522 SGASVYAGPRTGDDIICTENKSAATYTPDVYSQKRIARIRHASTSQITFTLSLDG 581

DB 520 SGAAVYRGPRTGDDIICTENKSAATYTPDVYSQKRIARIRHASTSQITFTLSLDG 579

QY 582 APNAYVFPDITKNGDITLVYNSFNLSAFTSPPELSC--NNLOIGVYGLAGKQVYIDKLE 639

DB 580 KAINQGNFSAITMRGDELDTKTRVGTFTTPEFLVOSTFTTGANNFSSGNEVYIDRIE 639

QY 640 FIPV 643

DB 640 FIPV 643

RESULT 14

C7AA_BACTU STANDARD; PRT; 1138 AA.

AC 003749;

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Pesticial crystal protein cry7Aa (insecticidal delta-endotoxin

DE CryII(a)) (crystalline entomocidal protoxin) (129 kDa crystal

DE protein).

GN CRY7AA OR CRYII(A) OR CRYIIIC.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RP SEQUENCE FROM N.A.

RA MEDLINE=92384571; PubMed=1514800;

RT Lambert B., Hofte H., Anys K., Jansens S., Soetaert P., Peferoen M.,

RT Novel Bacillus thuringiensis insecticidal crystal protein with a

RT silent activity against coleopteran larvae.

RL Appl. Environ. Microbiol. 58:2536-2542(1992).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS

CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE

CC AFTER AN IN VITRO SOLUBILIZATION AND TRIPSIN ACTIVATION STEP.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF

CC THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-

CC TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC -----

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CC -----

CC EMBL; M64478; AAA22351.1; -

DR EMBL; A07236; CAA00646.1; -

DR HSSP; P07130; IDIC.

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin.1.

KW Toxin; Sporulation.

SO SEQUENCE 1138 AA; 129391 MW; 6908676D4F6A1PAC CRC64;

Query Match 33.8%; Score 1152.5; DB 1; Length 1138;

Best Local Similarity 37.7%; Pred. NO. 4.9e-68;

Matches 255; Conservative 114; Mismatches 235; Indels 73; Gaps 19;

QY 1 MNPNNRSEHDTKTENNEVPNNHYQYLAEPNPLEDLANKKEFLMADNNTALUSS 60

DB 1 MNLNMLDGE-----DSNRLNLSNLTPTQKALSSIKMMNQDLSTIERQPPALASG 55

QY 61 TRKDVIOKISVGDGLGVCPFGCALVSFTNLTNLTWSEDP-WKAFMEQVEALMDQ 119

DB 56 NT--AINTVSYTGATLSALGVGASFTTNFYLKTAGLMPENCKIMDEPMEVEALIDQ 113

QY 120 KIADYAKNKALAELOGLONNVEDYVLSWSW---OKNPVSSRNPHSGRIEPLSQASH 176

DB 114 KIEEYRNKNAIMEDLGSLADKYKALADMGKDDPEALISVATERI-----IDSL 167

QY 177 FNSMPSFAISGEVLEFLLTAAQANPHFLKDAQIIGEEMGEKEDIAPFYKQLKLT 236

DB 168 FEFMSPEFVETGEIPLTLVYQAANLHALLRDLSTLGDKMGFTQNNIENYNNQKRI 227

QY 237 OEYDHCYKMYVNGLDKLGSSSEWVFNRRRMTLVLDLALFELYRLKPEVK 296

DB 228 SEYSDHCKWVNSGLSRNGSTYEQWVNNRRRMILMALDLAVFPHDPRRYSMETS 287

QY 297 TELTRDVLDPF-VGVNMLRGYGTFTSNLEN-YIRKPHLPYLRHIOPT-----RF 346

DB 288 TQLTREVTLDVPSLSISN-POIGSPFSQMENTALITPLVLDLDELTYITKRAFSHEI 346

QY 347 OPGYTGNDSPNWSGNYSTRPSISNDIITSPEYKNSSEPVON--LENGEKYRAVA 404

DB 347 OPLDF-----YMSAHKYSFKKSEQSN-LYTTGIYG-KTSGYISSGAVSFHNDIYRTLA 398

QY 405 NTLNLAWPSAVYSGVTKYEFQYNGQDEASTQYDSCRANNGANSMDSDIDLPETIDEP 464

DB 399 APSVAVVYPTQNYGVEQVEYGVKGVHVRGDNKYD-----LYTSIDQLPPD--GEP 449

QY 465 LEKGYSHOLNVMCFILMOG---SRGTIPVLMTNHSKVDFFNMIDSKITOLPLKAVKIQ 521

DB 450 IHEKTYHRLCHNATAFKSTPDYDNATIPFSTWHSATYKRIYKRIKTPAVKMKRLD 509

QY 522 SGASVYAGPRTGDDIICTENKSAATYTPDVYSQKRIARIRHASTSQITFTLSLDG 581

DB 510 DSTVYKPGPRTGDDIICTENKSAATYTPDVYSQKRIARIRHASTSQITFTLSLDG 581

QY 582 APENQYDCK-----TINKGDTLVYNSFNLSAFTSPPELSC--NNLOIGVYGL 627

DB 561 GOFNVTYINDKTLTQKFPNTVETTIGEGDLVYGSFGYESTTIOFPDEHRTKLHSDL 620

QY 628 SAGDKVYIDKIEFIPVN 644

DB 621 SNNSFYVDISIEFIVD 637

RESULT 15

C9CA_BACTO STANDARD; PRT; 1157 AA.

AC 045733;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticial crystal protein cry9Ca (insecticidal delta-endotoxin

DE CryIXC(a)) (crystalline entomocidal protoxin) (130 kDa crystal

DE protein).

GN CRY9CA OR CRYIXC(A).

OS Bacillus thuringiensis (subsp. tolworthi).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1442;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RA STRAIN-BTS02618A;

RC MEDLINE=96141404; PubMed=8572715;

RA Lambert B., Buysse L., Decock C., Jansens S., Plens C., Seey B.,

RA Seurlink J., Van Audenheove K., Van Rie J., Van Vliet A., Peferoen M.,

RT "A Bacillus thuringiensis insecticidal crystal protein with a high

RT activity against members of the family Noctuidae."

RL Appl. Environ. Microbiol. 62:80-86(1996).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD

CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,

CC PUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST

CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORKS. NO

CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO

CC BEETLE.

Search completed: January 10, 2003, 11:06:49
Job time : 16 secs

```
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: 237527; CAA85764.1; -
DR HSP: P07130; IDLC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
DR Toxin: Sporulation.
KM Sequence 1157 AA; 129775 MW; C364391EF7FDEB8A CRC64;

Query Match 33.7%; Score 1149; DB 1; Length 1157;
Best Local Similarity 37.5%; Pred. No. 8.5e-68;
Matches 258; Conservative 126; Mismatches 230; Indels 74; Gaps 18;

OY 1 MNPNNRSEHDTIKTTEENNEVPTNHOVQPLAETPNPTLEDLNYKEPLRMFTADNTEALD-- 58
DB 1 MNRKNOMEYELIDAPHCPCSDDDYRPLASDENALQNNKYKDYLOMTDEDYTDSTYNP 60
OY 59 --SSTTKDVIQKGISVVGDLGVGPEPGALVSFTYNTINTPSEDP--WKAFMEQVE 114
DB 61 SLISGSDAVQVATLVVGRITGALGVFSGQIYSFYOFLLNTLMPVNDTAIMEAFMRQVE 120
OY 115 ALMOQKADYAKNAKALALQGLQNNVDYASLSNQKKNPVSSRNPHSGRIRLEFSQAE 174
DB 121 ELVNOQITTEFARNQALALQGLQSDENVYQSRQNNLADNDTRN--LSVRAQFTALD 177
OY 175 SHFNNSPSPFASISGEVLEFTTYQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLK 234
DB 178 LDFYNALPLFAVNGQVPLSLVYAQAANLHLLKLLKSLFGBGMGFTQGEISTYIDROLE 237
OY 235 LTOEYTDHCYKWNVGLDKLRGSSYESWVNFNRYRREMTLVLDLALPPLVYRLYPE 294
DB 238 LTAKYTYNCETWYNTGLDRLRGTTESMLRYHQFRREMTLVLDVVALFPYDYDRLYPTG 297
OY 295 VKTELTEDVLTDPY-----GVNLRGCGT-----TESNIEN-YIRKPHLFDYLARIQFHT 344
DB 298 SNPOLTREVTDPVFNPPANVGLCRWGNTPVNTSELENAFIRPHPLDRLNLSLTISS 357
OY 345 RFQPGYGNDSFNWYSGNVSTRPSIGSNDIITSPEYG-----NKSEPVQNLFPN 395
DB 358 NRFP--VSSNFMQWMSGH--TLRSYLANDSAVEDSGLTTRATINPGVDGTRNREST 413
OY 396 GEKYRAVANTNLAVPSAVYSGVTKEF--SOYNDQDEASTQYDSKRNAGAVSWS 452
DB 414 AVDFRSALI-----GIY-GVNRASFVPGCLFNCTSPANGCGRD-----LYDT 455
OY 453 IDOLPP-ETTDEPLEKGYSHQNLVWCFMQ-----GSRGTIPVLWTWTKSVDFENMI 504
DB 456 NDELPPDESGTSS-----THRLSHVTFFSPOTNAGSIANAGSVPTVWTRDVLNNTI 510
OY 505 DSKRTIQLPLKAYKLAGSASVAVPFTGDIIOCTENGSAATIVTTPVSYSOKYRAR 564
DB 511 TPNRTIQLPLKASAPVSGTTLKPGFTGGILRTTNGTFTGLRVTVNSPLTQVRLR 570
OY 565 IHVASTQITFTLSLDGAPFNQYTFDKTINKGDTLYNSFNLSFST-----PFEISGN 618
DB 571 VRFASTGNFSIRVLGCVSICDVRLGSTMNGOELTFESEFTTREFTTTGPFPNPFPTQA 630
OY 619 N--IQIGVTGLSAGDKYIDKIEFIPVN 644
DB 631 QEILTVNAGVSTGGEYIDRIETIPVN 658
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:03:39 ; Search time 38 seconds
(without alignment)
3491.956 Million cell updates/sec

Title: US-09-943-692-2
Perfect score: 3406
Sequence: 1 MNPNNRSEHDITKTENNENV.....TGLSGDKVYIDKIEFIVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeoph: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	2	Q956N9
2	1175	34.5	719	2	Q9F0P8
3	1155	33.9	719	2	Q93N75
4	1154	33.9	719	2	Q85796
5	1111	32.6	1228	2	Q93775
6	1108	32.5	1228	2	Q93N75
7	1088	31.9	645	2	Q95603
8	1006.5	29.6	638	2	Q87654
9	988	29.0	1144	2	Q45745
10	980	28.8	1155	2	Q95296
11	974.5	28.6	1118	2	Q94M83
12	972	28.5	1155	2	Q93721
13	954.5	28.0	1180	2	Q955V8
14	944.5	27.7	1189	2	Q91877
15	942.5	27.7	620	2	Q45720
16	942.5	27.7	1176	2	Q45736

17	935	27.5	1176	2	Q9RC30
18	902	26.5	1118	2	Q9AM82
19	891	26.2	1171	2	Q06894
20	883.5	25.9	1176	2	Q9S514
21	882	25.9	1174	2	Q45749
22	847	24.9	1177	2	Q45735
23	842.5	24.7	1178	2	Q9R826
24	841	24.7	607	2	Q45721
25	841	24.7	618	2	Q45737
26	841	24.7	723	2	Q9S4B5
27	841	24.7	1177	2	Q03743
28	839.5	24.6	618	2	Q03206
29	839.5	24.6	1178	2	Q45768
30	835.5	24.5	1160	2	Q937F9
31	826	24.3	1118	2	Q9AM81
32	800	23.5	660	2	Q8R0V6
33	704	20.7	381	2	Q45740
34	693.5	20.4	1280	2	Q8VUK9
35	684	20.1	1236	2	Q939Y3
36	637	18.7	1128	2	Q9FDC0
37	613	18.0	1254	2	Q8VUL0
38	603	17.7	650	2	Q8VNX2
39	589.5	17.3	666	2	Q8VW62
40	569.5	16.7	1155	2	Q9AM80
41	526	15.4	688	2	Q8VNX1
42	504.5	14.8	1270	2	Q8VUL1
43	342.5	10.1	297	2	Q45789
44	271	8.0	50	2	P81518
45	248.5	7.3	723	2	Q9EVR2

ALIGNMENTS

RESULT 1

ID Q956N9 PRELIMINARY; PRT; 652 AA.

AC Q956N9; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Cry3Aa protein.

GN CRY3A.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

CC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BT22;

RA Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;

RT "A novel cry3Aa gene";

RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ237900; CAB41411.1; -.

DR HSSP: P07130; IDIC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

SQ SEQUENCE 652 AA; 74035 MW; 544AE16E1DFF647 CRC64;

Query Match 100.0%; Score 3406; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.2e-220;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVPTNHOYPLAETPNPTLEDLNYKEFLRTMTAANNFEALSS 60
DB 9 MNPNNRSEHDITKTENNENVPTNHOYPLAETPNPTLEDLNYKEFLRTMTAANNFEALSS 68
QY 61 TTKDVIQKISVYVGGDLGVGFPFGALVSFTYNLTNPSEDPWKAFFMEQVEALMDOK 120
DB 69 TTKDVIQKISVYVGGDLGVGFPFGALVSFTYNLTNPSEDPWKAFFMEQVEALMDOK 128
QY 121 TDIYAKKRALAELQGLNNVEYVSAIWSQKNPVSSRNPHSGKTRIRLFQASHPFNS 180

Db 129 IADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAESHRRNS 188
 QY 181 MPFAISGEVLEFITYAOANTHLFLKDAQIYGEEMGEKEIDAEFYKROLTOEYT 240
 Db 189 MPFAISGEVLEFITYAOANTHLFLKDAQIYGEEMGEKEIDAEFYKROLTOEYT 248
 QY 241 DHCVKMYWGLDKLRGSSYESSWVNFNRRBMTLVLDLALFPLDYVRLYPKEVKTETL 300
 Db 249 DHCVKMYWGLDKLRGSSYESSWVNFNRRBMTLVLDLALFPLDYVRLYPKEVKTETL 308
 QY 301 RDVLDPFVGVNMLRGYTTTSNIENTYRKPHLFDYLRHIOFHTRPQGYGNDSEFYMS 360
 Db 309 RDVLDPFVGVNMLRGYTTTSNIENTYRKPHLFDYLRHIOFHTRPQGYGNDSEFYMS 368
 QY 361 GNYSTRISGNDIITSFPGKNSSEPVONLEFNGEKYRAVANTMLAVPMSAVYSGYT 420
 Db 369 GNYSTRISGNDIITSFPGKNSSEPVONLEFNGEKYRAVANTMLAVPMSAVYSGYT 428
 QY 421 KVEFSQYNDQDEASTQTYDSKRNVAWSIDQLPEPTDEPLEKGYSHQNLVYMCFL 480
 Db 429 KVEFSQYNDQDEASTQTYDSKRNVAWSIDQLPEPTDEPLEKGYSHQNLVYMCFL 488
 QY 481 MGSRGITPVLTWHKSVDFENMIDSKITQPLVKAAYKQSGASVYAGPFTGGDIQC 540
 Db 489 MGSRGITPVLTWHKSVDFENMIDSKITQPLVKAAYKQSGASVYAGPFTGGDIQC 548
 QY 541 TENSAAITVTPVYSOKYRAHIASTQITFTSLDCAFPNOYFDTKNGDPLT 600
 Db 549 TENSAAITVTPVYSOKYRAHIASTQITFTSLDCAFPNOYFDTKNGDPLT 608
 QY 601 YNSFNLSFSTPFELSGNNLQIGVTLGASGDKYVYIDKIEFIPVN 644
 Db 609 YNSFNLSFSTPFELSGNNLQIGVTLGASGDKYVYIDKIEFIPVN 652

RESULT 2

Q9F0P8 PRELIMINARY; PRT; 719 AA.
 ID 09F0P8
 AC 09F0P8
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CRY11.
 GN CRY11.
 OS Bacillus thuringiensis.
 OG Plasmid pBTG19.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BTC007;
 RA Song F., Zhang J., Huang D., Li G.;
 RT "The cloning of a novel cryII gene from Bacillus thuringiensis
 strain..."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF211190; AAG43526.1; -
 DR HSP: P02965; ICY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Plasmid.
 SQ SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 34.5%; Score 1175; DB 2; Length 719;
 Best Local Similarity 39.0%; Pred. No. 1.7e-70;
 Matches 260; Conservative 126; Mismatches 234; Indels 46; Gaps 17;

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTTEA 56
 Db 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTTEA 56
 QY 57 LDSSTYADVIOKGISVVGDLGVGPPGALVSEFYNTPLNTWP-SEDPKAKMEQVEA 115
 Db 57 LDSSTYADVIOKGISVVGDLGVGPPGALVSEFYNTPLNTWP-SEDPKAKMEQVEA 115

Db 51 IDPFVASTIQTGIGIAGILGTGVPFAGQIASLSTFLLGELMPKGSQWEIFMEHVE 110
 QY 116 LMDOKIADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAES 175
 Db 111 LMDOKIADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAES 167
 QY 176 HFNNSMPFAISGEVLEFITYAOANTHLFLKDAQIYGEEMGEKEIDAEFYKROLT 235
 Db 168 LFOYKLPFAISGEVLEFITYAOANTHLFLKDAQIYGEEMGEKEIDAEFYKROLT 227
 QY 236 TOEYTHCVKMYWGLDKLRGSSYESSWVNFNRRBMTLVLDLALFPLDYVRLYPKEV 295
 Db 228 TSQYSHCVKMYWGLDKLRGSSYESSWVNFNRRBMTLVLDLALFPLDYVRLYPKEV 287
 QY 296 KTELTDVLDLPFVGVNMLRGYTTTSNIENTYRKPHLFDYLRHIOFHTRPQGYGNDSE 343
 Db 288 TSQYSHCVKMYWGLDKLRGSSYESSWVNFNRRBMTLVLDLALFPLDYVRLYPKEV 347
 QY 344 -TRFOPGYGNDSEFYMSGNYSTRISGNDIITSFPGKNSSEPVONLEFNGEKY 400
 Db 348 LSRMSNTQY---MNMGGHRLER-TIGG--VLNSTRGSGTNTSINPV-TLPFTSRDY 399
 QY 401 RAVANMLAVPMSAVYSGYTKVEFSQYNDQDEASTQTYD-SKRNVAWSIDQLPE 459
 Db 400 RTESLAGLMLFLTPQVNGVPRVDFHKKFATLPIASDNFYLGYAGYQLQDSENELPE 459
 QY 460 TTEPLEKGYSHQNLVYMCFLMGSRGITPVLTWHKSVDFENMIDSKITQPLVKAAY 519
 Db 460 TTEPLEKGYSHQNLVYMCFLMGSRGITPVLTWHKSVDFENMIDSKITQPLVKAAY 517
 QY 520 LOSGASVAGPFTGGDIQCETENGSAATVTPVYSOKYRAHIASTQITFTSL 579
 Db 518 LOSGASVAGPFTGGDIQCETENGSAATVTPVYSOKYRAHIASTQITFTSL 577
 QY 580 DGAPFNOYFDTKNGDPLTNSFNLSFSTPFELSG--NNLQYVGLSAGDKYVYIDK 637
 Db 578 NGKAINQGNFSATMNGEDLDYKTFRTVGTTFPFESFVQSTFTIGAMFSSGNEYIDR 637
 QY 638 IEFIVP 643
 Db 638 IEFIVP 643

RESULT 3

Q93NT5 PRELIMINARY; PRT; 719 AA.
 ID 093NT5
 AC 093NT5
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE CRY11A.
 GN CRY11A.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song F., Zhang J., Gu A., Huang D., Li G.;
 RT "A novel CryIIA endotoxin..."
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF373207; AAK66742.1; -
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 719 AA; 81225 MW; C629D72C44827241 CRC64;

Query Match 33.9%; Score 1155; DB 2; Length 719;
 Best Local Similarity 38.0%; Pred. No. 3.8e-69;
 Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTTEA 56
 Db 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTTEA 56
 QY 57 LMSSTYADVIOKGISVVGDLGVGPPGALVSEFYNTPLNTWP-SEDPKAKMEQVEA 115
 Db 57 LMSSTYADVIOKGISVVGDLGVGPPGALVSEFYNTPLNTWP-SEDPKAKMEQVEA 115

OY	57	LDSSTKDVQKQISVYGDLIVGVPFGGALVSFTNLENTWP--SEDPKRAEMQVEA	115
Db	54	FVSAST---TGTGTGIAGKLTLGLTFVGAFQAVALSLFLIGELAMPGRKKMWEFMHVE	110
OY	116	LMQKITADYAKNNALALELQIANNVDVYSALSWMKNPYSSRNPHSQRIRELSQAES	175
Db	111	IINOKISTVARNNALDLDKLGIDGALLVAHYHDSLESWGN--RNRTRARSVVASQYIALEI	167
OY	176	HFRNSMPAISGEVLFETTYQAANTHLFLLKDQOIGEEMGYEKEDIAEYRKQLK	235
Db	168	MFOVKLPSPFAVSGEEVPLLETYYQAANLHLLLRDAISFEKGWGLSSSELSTFFYNQVER	227
OY	236	TOEYTHCVMYNYNGDLKLGSSSVSNVRNRYBREMTLVLDLLEPLDYRLPKREV	295
Db	228	ACGDISDCVAMYSTGLNGLNGTAINESVARYNOERRDITLMLVDLVALFPSTDTQMPIKT	287
OY	296	KTELIRDLVTDPYGVNNLKRGYT-----FSNIE-NYIRKPHELYLHRIOFH--	343
Db	288	TAQITREYTDALIGTVHPHSFTSTTWXNNAPSFSAIEAAVRRNPILDLEQVITYSL	347
OY	344	-TRQPQCYGSDSNYNSGMYSTRBSIGSNDIITSFYFNKSKSEPQNLEFNGEVYRA	402
Db	348	LSRMSNTQY----NMWGCHKLEPR-TIGGTLANSTGSGTNTSINPV-TLPFTSRQVYRT	401
OY	403	VANNNLVMPSPVASGVTAYKEFS-QVYDQDEASTQYDSCRNVGASMSIDOLPEPT	461
Db	402	ESLAGLNFELTHPNVNGPVRPDVFMKFKPTHNPILASNFTYPGYAGIGLOLOSENELEPEAR	461
OY	462	DEPLEKGYSHOLANYMCFLMOGSRGITPVLTWHKSYDFENMDISKRTQLPLVKAJKIQ	521
Db	462	GOPYVESYSHRLSHI--GLISASHVKALYAVSWTHRSADRNTTEPSNIOTIPYKAFNLS	519
OY	522	SCASVAVAPRTGGDIITQCENGSAATIIYTPDVYSOKTRARVHA5TSQINFETLSQG	581
Db	520	SGAADVVRPPGTGGDILKRNTGTGFGDIRVININPEAQRVRRARRASTDLDLQFHTSING	579
OY	582	APFQNYEDKINKGDTLVYNSFMILASFSTPFELS--NNILOGVTLGSAGDKYIIDIK	639
Db	580	KAINQNGNSATIMNNGEDLDYTFPTVCTPTPTFSPRLVDQSFTTGIANWFSSGNEIYIDRIE	639
OY	640	FIVP 643	
Db	640	FVVP 643	
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RESULT 4			
ID	085796	PRELIMINARY:	PRT; 719 AA.
AC	085796;		
DT	01-NOV-1998 (TREMBLrel_08, Created)		
DT	01-NOV-1998 (TREMBLrel_08, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel_19, Last annotation update)		
DE	Insecticidal protein.		
GN	CryVI101.		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Plasmid large plasmid.		
CC	Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;		
OC	Bacilliaceae; Bacillus.		
OX	NCB1_TaxID=29339;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-S101;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF076953; AAC26910.1; -		
DR	HSSP: P02963; ICIT.		
DR	InterPro: IPR001178; Endotoxin.		
DR	Pfam: PF00555; endotoxin; 1.		
KW	Plasmid.		
SO	SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;		

OY	1	MNPNNRSHDITKTEN-NEVPTNHVOPLAETPPT--LEDLWKEFLPMATADNNTGA	56
Dd	1	MLKNQDDHOSSTSNAKVDKISTDLK-----NETDIELONIHEDCLKSEYEVEP	53
OY	57	LDSSTKVIVIGKISVAGDGLGVVFPPGALVSFYTNFNLINP-SEDPMKAFMEQVEA	115
Dd	54	FVSAST----IQTGICIAKKICTLTGLVPAGOVASLXSLFGELMWKGNQMIFEMHDE	110
OY	116	IMDKRIADYANKRALAELOGLQNVEDYVALSSMOKNPNVRNPHSGGRILEFSQAES	175
Dd	111	IINOKISTYARKKALTJDKGLDALAYVHSDLESWG--RNMRARSVVSQYIALEL	167
OY	176	HPRNSMPSPAISGVAVLELTTPYAQAANHLPLKAOYIGEEMGEKEDIAEFYROKL	235
Dd	168	MEVQKLPSPASVGEERPLPIYAQAANHLPLLRDSISTEGKMGLSSSSTIFTNRÖVER	227
OY	236	TOEYTDHCWKMYNVGIDLKSSSYESWVENFNRYRRBMTLVLDLIALFPLYDVRLYPKEV	295
Dd	228	AGDYSDHCYKWYSTGINLNRTNAESWVKYNQFRDMTLMVLIDLVALFPSYDTOMYPIKT	287
OY	236	KTELTRDVTLDPIYGVINNRIGYGT-----TSNIE-NYIKRPHELDYLHRIOFH--	343
Dd	288	TMOLTRREVYTDAIGVYHPHSPTSTTWNNAPSPSAIEAAVARNPHLDLFEOVITYSL	347
OY	344	-TRPOPGYGYNDSPFWMSGNYSTRPSISNDITSPFXGNKSSEPQUMLENGEKERYA	402
Dd	348	LSRMSTQY---MMNGGHKLEFR-TIGGLINISOTGSNTINSINV-TLPTSROYVTT	401
OY	403	VANTILAWPSAVYSQVTKVEFS-QYNDQTEASTOYTYSKRNVGAVSWSDISDOLPEFTT	461
Dd	402	ESIAGINFLFLOPVNGVPRVDEHMFKVTPRIASDNFYGYAGIGQLODSENELPREAT	461
OY	462	DBPLEKYSHOINYVACFMLOSQRGITPLWTMHKSVDFNMIDSKKITQLPVLKARYKO	521
Dd	462	GCPNYESYSHRLSH--GLISASHVAKALYSYTHREADTNTTERPSTOIPIYKAFLNIS	519
OY	522	SGASVVGAFRETGGDIIOCTENGSAATYYVDPVYSQYRARIRHYASTSQITFTVLSLG	581
Dd	520	SSAAVVRGCGEFGDILRRNTGTGFDDIVNIKPRAEPARVARIRASTDLOFHTSING	579
OY	582	APPNOVYEPFKTIKGDTLLYNSFNLASFSFPPELSC--NNLOGVMGLSAGDKVYIDKIE	639
Dd	580	KAINQNFSAVMKRGHDLDKTFRTVYGFYTPSFLLDYOSTFTTGAMNFSSEGENYIIDRIE	639
OY	640	FIPV 643	
Dd	640	FVPV 643	
 RESULT 5 093T75 PRELIMINARY: PRT; 1228 AA.			
ID	093T75:		
AD	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
De	Delta-endotoxin CryIIa2.		
GN	CryIIa2.		
OS	Bacillus thuringiensis (subsp. entomocidus).		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;		
OC	Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1436;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN-HD-9.		
RT	Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;		
RT	"Characterization of cryII gene and its flanking regions cloned from		
RT	Bacillus thuringiensis subsp. entomocidus HD-9."		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF363025; MAK51084.1; -		

DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139621 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 32.6%; Score 1111; DB 2; Length 1228;
Best local similarity 38.2%; Pred. No. 7.7e-66;
Matches 255; Conservative 117; Mismatches 238; Indels 58; Gaps 21;

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OY 1 MNPNNRSEHDITKTENNEVPTNHVQYPLAETNPTELDNYKEFLRTADNTEALDSS 60
DB 1 MTSNRKNEENIINAVSHSQAQMD-----LLPDAIETSLCIAENNNIDPPVSA 48
OY 61 TTKDVIOGKISVVDLGVGPPFGALVSFTYNTLTP--SEDPKAFMEQVEALMDQ 119
DB 49 ST---VQTGINAGRIIGLVGFPAQGLASFGLVGLMELPRGRDQWEIFLEHVEQLINQ 105
OY 120 KIDYAKKKAALAELOGLONNVEDYVSAIWSQKNPVSRRNHSGRTRE--LFSC---AES 175
DB 106 QITENAKRTALARKLQGLSDSFRATQOGLDLEN--RDDARRSVLYTYQYIALEL 158
OY 177 FRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEXEREDIAEFYKROLKLT 236
DB 160 FLNAMPFLFAIRNOEVLPLMAYAAANLHLRLDASLFGSEFGLTSQELQRYERYER 218
OY 237 QETDHCYKVNNGDLKLGSSYEVNFRKREMTLYVLDIALFPLYDVRLYKREY 295
DB 220 RDSIDYCEVNTGNSLNGTNAASWVRYNQFRDLTLGLDVALFPSYDRTYPIINT 278
OY 297 TELTRDVLTDPI--VGVN--NLRGYGT---TFSNIE--NYIRKPHLFDYLRHQFHRFQ 347
DB 280 AQLTRVYTDALIGATGVNMAAMWYNNAPSFSAIEMAIRSHLDELFLQULTISA--S 337
OY 349 GYGNDSFNWGSNYSYSTRPSIGSNDITSPRYG--NKSEPVQNLFEKGKRYAVAN 405
DB 339 RNSNTRHMTYNGRTIOSRP--IGGG--LMTSTGATNTSINPV--TLRFASRDYRTESY 393
OY 407 NLAVMPSAVY----SGVTKEFSQYNDQ--TDEAS---QYTDSCRKNVAVSMDSIDOL 456
DB 395 GVILM--GIYLEPIHGVPRVRENTNPONISDGINYSQPYESP--GLQKDETEL 448
OY 458 PETTDEPLEKGYSHOLNYWCFMOSRGTIPLVLTTHKSVFFNMIDSKRTIOLPLVK 516
DB 450 PETTERPNESYSHRLSHGILQ--SRVNVPIYSMTHRSADRTNIGRNRTIOLPMAK 506
OY 518 YLQGSASVYAGRFTGGDIQCTENGSAATYYVPDVSYSOKYRARLHYASTSQITFT 576
DB 508 SELPGTGVYVRGPGFTGGDILRTNTGCGPIRVTVNGPLTORVIRIGFRYASTVDFEF 566
OY 578 LSLDGAPFNQYFEDKTIKNGDITLYNSFNLSFSTPELS--GNLQIGVTGTSADKYYI 634
DB 568 VSRGTTVNNFRFLRTMNSGDELKIGNFVRATFTTPTFTQIODITRTISIGLSNGEYV 626
OY 636 IKIEIIPV 643
DB 628 IKIEIIPV 635

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RESULT 6

O93NM5 PRELIMINARY; PRT; 1228 AA.
AC O93NM5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE CRI1BA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;

RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF368257; AAK63251.1.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139666 MW; E86D9842341FB439 CRC64;

Query Match 32.5%; Score 1108; DB 2; Length 1228;
Best local similarity 38.3%; Pred. No. 1.2e-65;
Matches 256; Conservative 115; Mismatches 238; Indels 60; Gaps 22;

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OY 1 MNPNNRSEHDITKTENNEVPTNHVQYPLAETNPTELDNYKEFLRTADNTEALDSS 60
DB 1 MTSNRKNEENIINAVSHSQAQMD-----LLPDAIETSLCIAENNNIDPPVSA 48
OY 61 TTKDVIOGKISVVDLGVGPPFGALVSFTYNTLTP--SEDPKAFMEQVEALMDQ 119
DB 49 ST---VQTGINAGRIIGLVGFPAQGLASFGLVGLMELPRGRDQWEIFLEHVEQLINQ 105
OY 120 KIDYAKKKAALAELOGLONNVEDYVSAIWSQKNPVSRRNHSGRTRE--LFSC---AES 175
DB 106 QITENAKRTALARKLQGLSDSFRATQOGLDLEN--RDDARRSVLYTYQYIALEL 158
OY 176 FRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEXEREDIAEFYKROLKLT 235
DB 159 DELNAMPFLFAIRNOEVLPLMAYAAANLHLRLDASLFGSEFGLTSQELQRYERYER 218
OY 236 TOETDHCYKVNNGDLKLGSSYEVNFRKREMTLYVLDIALFPLYDVRLYKREY 295
DB 219 TRDSIDYCEVNTGNSLNGTNAASWVRYNQFRDLTLGLDVALFPSYDRTYPIINT 278
OY 296 KTELTRDVLTDPI--VGVN--NLRGYGT---TFSNIE--NYIRKPHLFDYLRHQFHRFQ 347
DB 279 SAQLTRVYTDALIGATGVNMAAMWYNNAPSFSAIEMAIRSHLDELFLQULTISA--S 337
OY 348 PGYGNDSFNWGSNYSYSTRPSIGSNDITSPRYG--NKSEPVQNLFEKGKRYAVAN 405
DB 338 RNSNTRHMTYNGRTIOSRP--IGGG--LMTSTGATNTSINPV--TLRFASRDYRTESY 393
OY 406 NLAVMPSAVY----SGVTKEFSQYNDQ--TDEAS---QYTDSCRKNVAVSMDSIDOL 456
DB 394 AGVILM--GIYLEPIHGVPRVRENTNPONISDGINYSQPYESP--GLQKDETEL 448
OY 457 PETTDEPLEKGYSHOLNYWCFMOSRGTIPLVLTTHKSVFFNMIDSKRTIOLPLVK 516
DB 449 PETTERPNESYSHRLSHGILQ--SRVNVPIYSMTHRSADRTNIGRNRTIOLPMAK 506
OY 517 AYKQGSASVYAGRFTGGDIQCTENGSAATYYVPDVSYSOKYRARLHYASTSQITFT 576
DB 507 ASELPGTGVYVRGPGFTGGDILRTNTGCGPIRVTVNGPLTORVIRIGFRYASTVDFEF 566
OY 577 LSLDGAPFNQYFEDKTIKNGDITLYNSFNLSFSTPELS--GNLQIGVTGTSADKYYI 634
DB 567 VSRGTTVNNFRFLRTMNSGDELKIGNFVRATFTTPTFTQIODITRTISIGLSNGEYV 626
OY 635 IKIEIIPV 643
DB 627 IKIEIIPV 635

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RESULT 7

O9S603 PRELIMINARY; PRT; 645 AA.
AC O9S603;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 GN CRUX GENE.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9408596; PubMed=8262221;
 RA Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,
 RT "Primary structure of the cryX** the novel Delta-endotoxin-related
 RT gene from Bacillus thuringiensis ssp. galleriae.";
 RL FEBS Lett. 336:79-82(1993).
 DR EMBL: X75019; CAA52927.1;
 DR HSSP: P07130; IDC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 FT NON_TER
 SQ SEQUENCE 1144 AA; 12939 MW; 7D28594A19C4B065 CRC64;

Query Match 29.0%; Score 988; DB 2; Length 1144;
 Best Local Similarity 35.4%; Pred. No. 1.3e-57;
 Matches 229; Conservative 117; Mismatches 237; Indels 64; Gaps 17;

41 NYKFLMTADNNTTEA-LDSSTKDYIOGIGVGDLDGVGFPFGALVSPYTNFLMTI 99
 19 SYDKLMKSGDYIDYINPGVNRGLQGDIDVAVVYVAGLGGPVGGLTGLTGLTGL 78
 100 WPEDEP--WKAFMEVYEAALMDKDIADYAKKLAELQGLQNNVEDYVSAALSMQKNPVSS 157
 79 WPSNDAVWEAFLEQMEELIEQRIQSDQVAVTALDGLTQVYVYVYVYVYVYVYVYVYV 135
 158 RNHSQGRITRELSQAESHFRRNSMPSFAISG-----YEVLETTYQAQANHLTLDAQ 212
 136 -NGVRANLVLQRFELHAFVSSMPSFG-SGSGSQRFAQLVYVYVYVYVYVYVYVYVYV 193
 213 YGEEGKYKEDIABEYKQKL-TOEYTHCVKVVYVGLDKLKGSSYESVWVNFYRRE 271
 194 KTGARWGLRESQIGNLYENELQTRTDYTNHCYNVYVYVYVYVYVYVYVYVYVYVYVYV 253
 272 MFLTVLDLALPLVDVRLYKPEVTELRDYLDPDLYGVNN-----LRGYGT- 319
 254 ATLAMDIALPLPYNTRRYPLAVNPOLTRVYTDPL-GVPSSESSLEPBLRCLRMQETS 312
 320 --TFSTNEN-YIRKPHLDYLHRIQFHTRFQGYGNDSEFMYMGVYVSTPSSIGNDII 376
 313 AMTFSLERVAIISPHLDPTINMLITYGFSVHLTNQLEGMWLGHSVTSLSLAGPTTV 372
 377 TSPFGKNSSEPVQNLNENGEKVRVAVANTMLAV-WPSAVYGVYKVEF-----SOY 427
 373 LRRNKGSTTS-IVNYSFENDRDYVQINTRSHTGLGFQNAFLFGITRAQFPGGTYSVTR 431
 428 NDQTEASTQYVDSKRNVAWSMDSIDQLPETTDEPLEGYSQNLVYVWCFL-----MQ 462
 432 NALTCEQ-----NYSIDELPLDNEPLSKYSRHSLSHTSYLHVLTID 477
 483 GSR---GTIPVLTWTHKSVDFNMDSKKITQLPLVYKAYKLSGASVAVAPRFTGDIQ 539
 478 GINISGMLPTVYVWTHRDVLTNTADRLTQLPLVKSFEIPAGTIVVRPGFTGDIAR 537
 540 CENGSNATIVTPDVVSOKYRARIHASTSQTFTLSLDGAPNOYVYDKTINKGDTL 599
 538 RTGVGTFTIRRTAPLITORYRIRFRPASTTNLFIGIRGDRQVYVDFDGRITMNGDEL 597
 600 TYNSENLASFSTPELISGNNLQIGV--TGLSAGKVIYIDIEFIPV 644
 598 RYSPATREFPTDFNFQPOELLISVFANNAASAGOEYVFDIEITIPV 644

RESULT 10
 ID 09F296 PRELIMINARY; PRT; 1155 AA.
 AC 09F296;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Meza-Basso L.A., Theodoruz C.,
 RT "Cloning and expression of a delta endotoxin gene from a Chilean
 RT native Bacillus thuringiensis strain.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U94191; AG16877.1;
 DR HSSP: P02965; ICTY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 28.8%; Score 980; DB 2; Length 1155;
 Best Local Similarity 33.9%; Pred. No. 4.4e-57;
 Matches 225; Conservative 124; Mismatches 231; Indels 84; Gaps 19;

42 NPNNRSEHDTITKTENNEVYTNHVOYPLAEPNPLLEDLANKLEFLMTADNNTALDST 61
 4 NPN-----INECIPNCLIS-----NPEVEVLGE--RIETGYTPIDISL 42
 62 TKVDYIOGIGVYVGDLDGVGFPFGALVSPYTNFLMTI-----PSEDPKAFMEQVYALM 117
 43 TQPLSEFPVPGAGFVGLV-----DITWGLFGSQ--WAFVYVQIQLI 84
 118 DQKIDYAKKLAELQGLQNNVEDYVSAALSMQKNPVSSNHPHSGRIRLEFSQASHF 177
 85 NORIEEFARNAQMSIRLEGSNLYQYVASFREMEADPT--NPALREEMRIQFDMNSAL 141
 178 RNSMPSFASGVEVLETTYQAQANHLTLDAQIYGEEMKYKEDIABEYKQKLQ 237
 142 TTAIFLEFAVQNTQVPLLSVYVQVAAHLSTVLDVSVFGQRFMAATINSRYNDLRLIG 201
 238 EYTHCVKVVYVGLDKLKGSSYESVWVNFYRRETELTVDLALPLVDVRLYKPKVKT 297
 202 NTDHVAHRYNTGLERWVGPDSDRMIRYNQFRELITLVLDIVSLFPNYSTRTPYRTVS 261
 298 ELTRVDLDPYGVNNLKG-YGTFSNIENTYIRKPHLEDYLHRIQFHTRFQGYGNDSE 356
 262 QLTREIYVNPV--LENFGSFRSGAQIEGSIIRSPHMDILNSTITYVTDHAREY----- 314
 357 NWSGVNYSTRPSIGSNIIITSPFYGNK--SEEPQNLNEN-GEVYVAVANTMLAVWPSA 414
 315 -YWSHQIMASFPVSGSEPTTFLGTWGNAPQORIVAOIGGVYRTLSST---LYRRP 370
 415 YVSQYKVEFSQYNDQTEASTQYVDSKRNVAWSM-----DSIDQLPETTDEPLEG 468
 371 FNIGINNOQLSVL-DGTFEA---YGTSSNLPASVYKKSQTVSLDEIPQNNVPPRGG 425
 469 YSHQNTWYKCLMGSKRTI-----PVLVLTWTHKSVDFNMDSKKITQLPLVYKAYKLSG 523
 426 FSHRLSHVSMRSGFSNVSIIIRAPMFSWTHRSABEENIIPSSQITQPLFKSTNLGSG 485
 524 ASVAPRFTGDIITQENGSNATIVTPDVVSOKYRARIHASTSQTFTLSLDGAP 583
 486 TSVYKGPFTGDIILKRTSQGLTSLVNTAPLSQYRIRIRYASTTNLQFHTSIDGR 545
 584 FNQYVPDKTINKGDTLTYVSENLASFSTPELISGNNLQIGVNGLSA-----GDKYIDKI 638
 546 INQGNFATMSSGSLGSGSFRVYVGTTPPNFNGS---SVFLSAHAYVNSGNEVYIDKI 602
 639 EFIP 642

Db 603 EFVP 606

RESULT 11
ID 09AM83 PRELIMINARY; PRT: 1118 AA.

AC 09AM83: 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 19, Last sequence update)
DE Insecticidal crystal protein BPRX24.
OS *Bacillus thuringiensis* serovar *kunthax24*.
OC Bacteria; Firmicutes; *Bacillus*/Clostridium group; Bacillales;
OC Bacillaceae; *Bacillus*.
OX NCBI_TaxID=147284;
RN (1)
RP SEQUENCE FROM N.A.
RA Nagarathnam P., Xavier R., Jayaraman K., Murugan V.;
RT Characterization and full-length sequencing of insecticidal crystal
RT protein (cryI) of novel *Bacillus thuringiensis* subsp. *kunthax24* and
RT its specific toxicity towards three economically important pests;
RT *Spodoptera litura*, *Helicoverpa armigera* and *Plutella xylostella*.
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF327924; AAK14336.1; -
DR HSSP: P02965; ICIV.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin.1.
SQ SEQUENCE 1118 AA; 12681 MW; 33DA5B8C2CDF059D CRC64;

Query Match 28.6%; Score 974.5; DB 2; Length 1118;
Best Local Similarity 34.1%; Pred. No. 9.8e-57;
Matches 221; Conservative 125; Mismatches 230; Indels 73; Gaps 18;

QY 17 NNEPTNHQVPLAETNPFLDNTYKEFLMTADNTEALDSTSTQVOKGISVYGD 76
DB 8 NECPYNCLS-----NPEYVLCGE---RIETGYTPIDISLVLSEVPAGGFV 57
QY 77 LGVVFPGGALVSYTNFNTLTIW----PSEDPKAKMEQVEALMDOKIADYAKKALAE 132
DB 58 LGVL-----DIWIGIFGPGSQ--WDARLVQIEQLINQRIEFANQAIISR 99
QY 133 LOGLONNVEDYVSLSSMOKNPVSSRNPHSOGRIREFLSQAEHFNRSMSPFASIGEV 192
DB 100 LEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMSNALTALPLFAVQNOVP 156
QY 193 FLTYQAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROKLQEQETDHCVKYNGLD 252
DB 157 LLSYVQAANTHLVLRNDSYFGQRKGFDAATINSRINDLRLIGNTTDAHVRMYNGLE 216
QY 253 KLRGSSYEVNFRNRYRREMTLVLDIALPFLYDRLYPREKTELRDVLDPVIGVN 312
DB 217 RVMPDSDHMYRNOFRRELTFLVDIVSLPNDSTRYPPIRTVSQLTREIYTPV--LE 274
QY 313 NLRG-YGTFENIENYIRKPHLFDYLRIOFHTRFQCYGNDSPNWSGYSVTRSIG 371
DB 275 NFDSFSGSAGIGESIRSPHLMILNSTIYTAHREY-----YWSGQIMASPVGE 328
QY 372 SNDITSPFYGNK--SSEPVQMLEFN-GEKYRAVANTMLAVPASYVSGYKVFESYND 429
DB 329 SCPEPTFLVYTCMGNAQORIVAGLOGGVYRTLSST--LYRRPFGNGINQQLSVL-D 384
QY 430 QTEASTQYDSKRVAVSW-----DSIDQLPETTDEPLEKGYSHQNLVYMCFLMOG 483
DB 385 GTEFA---YGTSSMLPAAVYRKSGTVDSDLEIPONNNVPPRGFSHRLSHVSMFRSGF 440
QY 484 SSGT-----PVLWTHRSVDFPNMIDSKKITOLPLVKAAYLQSGASVAVAPRFGGII 538
DB 441 SSSVSITIRAPFWSIHSAEENNIIPSSQITQIPLTSLNGSGTSYVKKPGTGGDIL 500
QY 539 QCTENGSAITVYTPDVYSQKYRARIHYASTQITFTSLSDGAPFNQYEDKTIKNGDT 598
DB 501 RRTSGOISTLRVNTITATLSQRYRVARIRASTTNQFHTSIDGRPIINGNSATWSSGN 560

QY 599 LTYNSFNLASFTPELSCNNLQIGVTGLSA-----GDKVYIDKIEPIP 642
DB 561 LQSGAFMTVVGFTTFPNFSNGS---SVFTLSAHVFNSGNEVYIDRIEFVP 606

RESULT 12
ID 093721 PRELIMINARY; PRT: 1155 AA.

AC 093721: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Crystal protein CryIAb16.
OS *Bacillus thuringiensis* (subsp. *israelensis*).
OC Bacteria; Firmicutes; *Bacillus*/Clostridium group; Bacillales;
OC Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1430;
RN (1)
RP SEQUENCE FROM N.A.
RA Yu J., Tan L., Wu D., Pang Y.;
RT "Molecular characterization of a silent gene encoding a 130-kilodalton
RT crystal protein from *Bacillus thuringiensis* subsp. *israelensis*."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF375608; AAK55546.1; -
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin.1.
SQ SEQUENCE 1155 AA; 130747 MW; 7F0C98BE0100C7698 CRC64;

Query Match 28.5%; Score 972; DB 2; Length 1155;
Best Local Similarity 33.7%; Pred. No. 1.5e-56;
Matches 224; Conservative 123; Mismatches 233; Indels 84; Gaps 19;

QY 2 NPNRNBHDITKTENNPNTHQVPLAETNPFLDNTYKEFLMTADNTEALDST 61
DB 4 NPN-----INECPYNCLS-----NPEYVLCGE---RIETGYTPIDISLVL 42
QY 62 TKDVIQGISVVDLGVVGFPGGALVSYTNFNTLTIW----PSEDPKAKMEQVEALM 117
DB 43 TQFLSEFPVGAQFVGLV-----DIWIGIFGPGSQ--WDARLVQIEQLI 84
QY 118 DQIADYAKKALAELOGLONNVEDYVSLSSMOKNPVSSRNPHSOGRIREFLSQAEHF 177
DB 85 NORIEEFARQAIISRLGSLNLYQIYAESFREWEADPT--NPALREEMRIQFNDMSN 141
QY 178 RNMPSPFASIGEVFLTYQAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROKLQ 237
DB 142 TTAIPLEFAVQNTYRPLLSYVQAANTHLVLRNDSYFGQRKGFDAATINSRINDLRLIG 201
QY 238 EYTDHCYKMYNGLDKLRGSSYEVNFRNRYRREMTLVLDIALPFLYDRLYPREKTE 297
DB 202 NYTDHAVRWYNTGLERWGPDSRDWIRYNOFRRELTFLVDIVSLPNDSTRYPPIRTVS 261
QY 298 ELTRDVLDPVIGVNNLRG-YGTFENIENYIRKPHLFDYLRIOFHTRFQCYGNDSP 356
DB 262 QLTREIYTPV--LENFDGFSRGSAGIGESIRSPHLMILNSTIYTAHREY----- 314
QY 357 NYMSGNVSTRPSIGSNDITSPFYGNK--SSEPVQMLEFN-GEKYRAVANTMLAVPASA 414
DB 315 -YWSGQIMASPVGFSPEPTFLVYTCMGNAQORIVAGLOGGVYRTLSST--LYRRP 370
QY 415 VYSGVTKEVERSOYNDQTEASTQYDSKRVAVSW-----DSIDQLPETTDEPLENG 468
DB 371 FNIGINNQQLSVL-DGTEFA---YGTSSMLPAAVYRKSGTVDSDLEIPONNNVPPRG 425
QY 469 YSHQNLVYMCFLMOGSGT-----PVLWTHRSVDFPNMIDSKKITOLPLVKAAYLQSG 523
DB 426 FSHRLSHVSMFRSGFSNVSITIRAPFWSIHSAEENNIIPSSQITQIPLTSLNGSGT 485
QY 524 ASVAGPRFGGDIQCTENGSAITVYTPDVYSQKYRARIHYASTQITFTSLSDGAP 583

Db 486 TSVKGGFTGGDLRTSPGQISTLRVNTAPLSQRYRIRVASTTNLQFTSIDGR 545
 QY 584 ENOYEDKTKNGDITLYNSFNLSSTPELSENNLQIGVGLSA-----GDKYIDKI 638
 Db 546 INGNFSAITSSGSLNLSGSEFTVGGFTTTPNFNGS---SVFTLSAHVNSGNEYIIDI 602
 QY 639 EFIP 642
 Db 603 EFVP 606

RESULT 13

Q95SV8 PRELIMINARY; PRT; 1180 AA.

AC Q95SV8; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE BT84A1 crystal protein.
 GN BT84A1.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Nagamatsu Y.;
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
 RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
 thuringiensis subsp. dendrolimus T84A1.";
 RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
 RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
 thuringiensis.";
 RL Agric. Biol. Chem. 48:611-619 (1984).
 DR EMBL; AB026261; BAA77213.1; -
 DR HSSP; P02965; ICIV.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DC62D CRC64;

Query Match 28.0%; Score 954.5; DB 2; Length 1180;
 Best Local Similarity 33.7%; Pred. No. 2.4e-55;
 Matches 227; Conservative 118; Mismatches 224; Indels 105; Gaps 20;

QY 2 NNPNRSEHDITTEENNEVPYTHVOYPLAEPNPPTLEDLNYKEFLRTADNTEALDSST 61
 Db 4 NPN-----INCEIPYCLNLS-----NPEVEVLGGE---RIETGTPIDISL 42
 QY 62 TKDVIOKISVGDILGVVGFPGGALVSYTNPLNTIW-----PSEDPKAFMEQVEALM 117
 Db 43 TQFLSEVPAGAVGLV-----DIITGIGFPGSQ--WDAFLVQIOL 84
 QY 118 DOKIADYAKNALALQLOLQNNVEDYVALSSMOKNPVSSNPNRSGRIKRLFSQAESHF 177
 Db 85 NQRIEFARNOAISRLBELSLNLYOYIAESFREWEDP---NPLRREMRKQFDMNSAL 141
 QY 178 RNSMSPFISGTYEVLFTTVYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQQLKLTQ 237
 Db 142 TTAAPLFAVQVYVPLSVYQOANLHLSVLRDVSFGQRMGFAATINSRYNDLTRLIG 201
 QY 238 EYTDICVQWYVGLDKLGGSSYSSVMNRRYRREMTLTVDLLLPLFYRLPYKREYKT 297
 Db 202 NYTDYAVWMTGLERWGPDSRDMWRVYNQPRRLTLVLIDIVALFSNYDSRRYPITVTS 261

QY 298 ELTRDVLDPPIVGNVNLNGYGT-----SNLENYTRKPLHLDYLRIQFHTRFQPGYCN 353
 Db 262 QLTREIYNPV-----LENFDSFSGMAORLEQNRQHLNDLNRITITYDVHNG----- 312
 QY 354 DSEFNWAGNYSTRPSISNDITTSPPYGNK--SEPPVONLEFNEGKYRAVANLWAVP 412
 Db 313 --FNWSGHQTASPVGSGPEFAFLPGNAGMAPVLYVLGIGIFRTLS----- 362
 QY 413 SAVY-----SG-----YKVEFSQYNDQTEASTQYIDSKRNAGVMSIDQLP 458
 Db 363 SPLRYRIILGSGPNNOELFVLDGTEFSFASLTINLPST---IYRQRTV--DGLDVP 416
 QY 459 ETTDEPLEKGYSHOLNYVCEFLMOGRGT-----PVLTWTKSGVDFPMDSKRTIOLP 513
 Db 417 QDNVPPRAGFSHRLSHT--MLSGAGAVYTLAAPTSMQHRSAERNINIPSSQITQIP 474
 QY 514 LKAVKLOSAGSVAGPFTGGDIIIOCTENGSAATYVDPVYSQRYRARIHYASTSQI 573
 Db 475 LTKSTNLGSGTSVWGPFTGGDILRTSPQISTLRVNTAPLSQRYRIRVASTTNL 534
 QY 574 TETSLDGAFFNOYFEDKTKNGDITLYNSFNLSSTPELSENNLQIGVGLSA----- 629
 Db 535 QFHTSIDGRPNQGNFSAITSSGSLNLSGSEFTVGGFTTTPNFNGS---SVFTLSAHVN 591
 QY 630 -GDKYIDKIEFIP 642
 Db 592 SGNEYIIDRIEFVP 605

RESULT 14

Q9L877 PRELIMINARY; PRT; 1189 AA.

AC Q9L877; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Toxin Cry1Ca6.
 GN CRY1Ca6.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A2-F;
 RA Yu J., Pang Y., Li J.;
 RT "Cloning and sequence analysis of the cry1Ca6 gene from Bacillus
 thuringiensis, strain A2-F.";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF215647; AAF37224.1; -
 DR HSSP; P02965; ICIV.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 27.7%; Score 944.5; DB 2; Length 1189;
 Best Local Similarity 35.2%; Pred. No. 1.1e-54;
 Matches 234; Conservative 113; Mismatches 226; Indels 91; Gaps 24;

QY 16 ENNEVPYTHVOYPLAEPNPPTLEDLNYKEFLRTADNTEALDSSTTKDVIOKISVGD 75
 Db 3 ENNO--NQCIPYCLNPEVEVLGGE---RISTGNSSIDISLIVQPLVSNFVGGGF 55
 QY 76 ILGVGFPFGGALVSYTNPLNTIMPSEDPKAFMEQVEALDOKIADYAKKALALQ 135
 Db 56 LVGLDIPVWG-----IVGPSQ--WDAFLVQIOLINERIAEFAARNAAANLLEG 101
 QY 136 LQNNVEDYVALSSMOKNPVSSNPNRSGRIKRLFSQAESHFRNSPSPASIGYEVLT 195
 Db 102 LGNNFNINIEAFKEWEDP---NNPATRTVIDRIRILDLGLERDIPSRISGFEVPLLS 158
 QY 196 TYQOANTHLFLKDAQIYGEEMGYEKEDIAEFYKQQLKLTQDYDHCYKWNVGLDKIR 255

Db 159 VVAQANLHLAILRDSVIFGERMGVTTINVENYNNLRIRHIDEYADHCANTYRGILNLP 218
 QY 256 GSSYESVNNRNRKREMTLVLDLALFPLVDRLPKVEKTLTDVLTPIGVN-NL 314
 Db 219 KSTYQDMITNRLRLDLTLVLDIAAFPNYDNRKRPDIQVGLTREVYDPLINPOL 278
 QY 315 RGYG--TTFENIE-NYIRKPHLEDYLHRIQFHTRFQPGYGNDSFN-----YSSGNVST 366
 Db 279 QSAQALPTEFNMSSALRNPHLDLNNLTFT-----DPSVGRNFYWGGRVTS 329
 QY 367 RPSIGNDITSPFYGNKSS-EFVONLENGEKYRAVANTNLAV---WPSAVYS-GV 419
 Db 330 SLIGGGN--ITSPYIGLEANQEPSTFTENG-PVFRILSPILRLAQPPAPPFNLRCY 386
 QY 420 TKPEFSQYNDQDEASTQYIDSKRNWAGVSWDSIDLPETTDEPLEKGYSHQNTVMCF 479
 Db 387 EGVEFS-----TPNSFTY--RGRQTV--DSELTELPEDNSVPREGYSHRL---CH 431
 QY 480 LMGSGRTIPVL-----THKSVDFENMIDSKKITOLPLVKAAYLQSGASVYAGPRFT 533
 Db 432 ATVQNSGRTIPVLTTGVFSMTHRSATLNTIDPERINQPLVGFVWGTSTVITGPGFT 491
 QY 534 GGDICTENGSAATYVTPDVYSQKYRARIHASTQITFTLSLDGAFN-----585
 Db 492 GGDILRNTRGDFVSLQVNNINSPIQRYRLRFYAS-SRDARIYVLGAASVGVGQVY 550
 QY 586 QYFEDTKINKGDTLYNSFNELASFSPPELISGNLQIGVT-----GISACDXYIDK 637
 Db 551 NMDLQITMEIGENLMTSTERYTDFNSNPFSEFRANDILGISERPLFGAGSISGE-LYIDK 609
 QY 638 IEFI 641
 Db 610 IEIT 613
 RESULT 15
 045720 PRELIMINARY; PRT: 620 AA.
 AC 045720;
 DT 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE CRYIA(a) (Fragment).
 GN CRYIA(a).
 OS Bacillus thuringiensis.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRD-12;
 RA MEDLINE-95386467; PubMed-7657602;
 RA Masson L., Mazza A., Gringorten L., Baines D., Anellunas V.,
 RT "Specificity domain localization of Bacillus thuringiensis
 RT insecticidal toxins is highly dependent on the bioassay system.",
 RT Mol. Microbiol. 14:851-860(1994).
 DR EMBL: U43605; AAA86265.1; -.
 DR HSSP: P02965; ICIX.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 FT NON_TER 1
 FT TER 620
 SQ SEQUENCE 620 AA; 69428 MW; 4571A095E565EDE CRC64;

Query Match 27.7%; Score 942.5; DB 2; Length 620;
 Best Local Similarity 33.4%; Pred. No. 5.7e-55;
 Matches 225; Conservative 118; Mismatches 226; Indels 105; Gaps 20;
 QY 2 NNNNRSEHDTITTEENNEPTNHQYPLAEFPNPLEDLNKEFRLMRADNTEALDSST 61
 Db 4 NPN-----INCEIPNCLS-----NPEVEYIGE--RIETGTPIDISL 42
 QY 62 TRDVIOKGISVVDLGVVFPFGALVSFYTNFNTMT-----PSEDPMKAFMEQVEALM 117
 Db 43 TQELISEFPVGAQFVLGLV-----DIIMGIGPQG--WDNFVQIDBLI 84
 QY 118 DOKIADYANKKLAELQIGANNVEDYVSAIISWQKNPVSSRNPHSGNIRELFSQASHF 177
 Db 85 NORIEEFARNQAIISRLGSLNLYQIYAESFREMADEPT--NPALREMRIOFNDMSAL 141
 QY 178 RSMSPFALSGVEVFLFTYAQANTHLFLKDAQYBEGNGEYEDAEFKRKLXLTQ 237
 Db 142 TTAIFLLAVQNTQVPELSTYVOANDLSVLNDVSPFGQRMGFDAATNSRYNDITRLIG 201
 QY 238 EYTDHCQKKNVNGDLKLRGSSYESVNNRNRKREMTLVLDLALFPLVDRLPKVEK 297
 Db 202 NYTDVAVRMYNTGLBRWMPDGRDWWVRVNOQFRELTLVLDIVALFSNYDSRRVYRTVS 261
 QY 298 ELTRDVLDPYIVANNLKCYGTF-----SNIEYIRKPHLEDYLHRIQFHTRFQPGYGN 353
 Db 262 QLTRELTYTPV-----LENFDSFRGMAQRIEONIROPHLMDILNSITYTDVHRC-- 312
 QY 354 DSEFNWGSQYVSTRPSIGNDITSPFYGNK--SSEPVONLENGEKYRAVANTNLAWP 412
 Db 313 --FNWSGHQITASPVGESGPEFAPPLFGNAGNAPVVALVSLTGIGIRTL-- 362
 QY 413 SAVY-----SG-----VTKVEFSQYNDQDEASTQYIDSKRNWAGVSWDSIDLP 458
 Db 363 SPLYRRIILGSGPNNQOELFVLDCTEFSPASLTNNLPSF-----IYRQRTV--DSLVDIYIP 416
 QY 459 ETTDEPLEKGYSHQNTVMCFMIGSSRGTT-----PVLWTHKSVDFENMIDSKKITOLP 513
 Db 417 QDNSVPPRAGFESHRLSHVY--MLSOAGAVVYLRAPTFSWQHRSAEFNNIIPSSQITQIP 474
 QY 514 LVKAYKLOGASVAVGPRPTGGDIIOCTENGSAATYVTPDVYSQKYRARIHASTSQI 573
 Db 475 LKSTNLSGGSIVKPGFTGDIILKRTSPGISTLRVNTAPLSQRYRVRIRASTNL 534
 QY 574 FTTLSDGAPFNQYFEDTKINKGDTLYNSFNELASFSPPELISGNLQIGVTGLSA----- 629
 Db 535 QFHTSIDGRPINQGNFSATMSSGSLNLOGSFRFTVGFTTTPNFSNGS---SVFTLSAHYFN 591
 QY 630 -GDXYIDKIEFIP 642
 Db 592 SGNEVYIDRIEFEP 605

Search completed: January 10, 2003, 11:07:35
 Job time : 42 secs

100

100

100

100

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 14:27:10 : Search time 40 Seconds
(without alignments)
2145.335 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644

Sequence: 1 MNNRNNREHFTITTENNV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

A_Geneseq_101002:*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	644	9 AAP70085	Sequence of toxin
2	644	100.0	644	9 AAP82487	Delta endotoxin en
3	644	100.0	644	10 AAP94679	Amino acid sequenc
4	644	100.0	644	10 AAP95585	M-7 crystal toxin.
5	644	100.0	644	14 AAP39751	Delta endotoxin.
6	644	100.0	644	15 AAR56697	CryIIIA insecticida
7	644	100.0	644	15 AAR56698	CryIIB insecticida
8	644	100.0	652	20 AAY23214	Amino acid sequenc
9	597	92.7	597	17 AAM00334	Bacillus thuringie
10	597	92.7	597	21 AAY69666	Wild-type Bacillus

11	595	92.4	610	11 AAR05537	Synthetic Bacillus
12	595	92.4	610	17 AAM00333	Bacillus thuringie
13	595	92.4	610	21 AAV69667	Bacillus thuringie
14	590	91.6	956	12 AAR15784	B. thuringiensis to
15	590	91.6	1100	17 AAR15783	B. thuringiensis to
16	543	84.3	644	17 AAR99960	B. t. coleopteran
17	543	84.3	644	18 AAW34811	Novel CryIIIA muta
18	543	84.3	644	18 AAW34812	Novel CryIIIA muta
19	543	84.3	644	18 AAW34813	Novel CryIIIA muta
20	543	84.3	644	18 AAW34814	Novel CryIIIA muta
21	543	84.3	644	18 AAW34815	Novel CryIIIA muta
22	543	84.3	644	18 AAW34816	Novel CryIIIA muta
23	543	84.3	644	18 AAW34817	Novel CryIIIA muta
24	543	84.3	644	18 AAW34818	Novel CryIIIA muta
25	543	84.3	644	18 AAW34819	Novel CryIIIA muta
26	543	84.3	644	18 AAW34820	Novel CryIIIA muta
27	543	84.3	644	18 AAW34821	Novel CryIIIA muta
28	543	84.3	644	18 AAW34822	Novel CryIIIA muta
29	543	84.3	644	18 AAW34823	Novel CryIIIA muta
30	543	84.3	644	18 AAW34824	Novel CryIIIA muta
31	543	84.3	644	18 AAW34825	Novel CryIIIA muta
32	543	84.3	644	18 AAW34826	Novel CryIIIA muta
33	543	84.3	644	18 AAW34827	Novel CryIIIA muta
34	543	84.3	644	18 AAW34828	Novel CryIIIA muta
35	543	84.3	644	18 AAW34829	Novel CryIIIA muta
36	543	84.3	644	18 AAW34830	Novel CryIIIA muta
37	543	84.3	644	18 AAW34831	Novel CryIIIA muta
38	543	84.3	644	18 AAW34832	Novel CryIIIA muta
39	543	84.3	644	18 AAW34833	Novel CryIIIA muta
40	543	84.3	644	18 AAW34834	Novel CryIIIA muta
41	543	84.3	644	18 AAW34835	Novel CryIIIA muta
42	543	84.3	644	18 AAW34836	Novel CryIIIA muta
43	543	84.3	644	18 AAW34837	Novel CryIIIA muta
44	543	84.3	644	18 AAW34838	Novel CryIIIA muta
45	543	84.3	644	18 AAW34839	Novel CryIIIA muta
46	543	84.3	644	18 AAW34840	Novel CryIIIA muta
47	543	84.3	644	18 AAW34841	Novel CryIIIA muta
48	494	76.7	610	16 AAR85982	Blt synthetic (Y2A
49	471	73.1	644	17 AAR99958	Bacillus thuringie
50	453	70.3	644	9 AAP80467	Bacillus thuringie
51	344	53.4	645	18 AAW34784	An artificial modi
52	300	46.6	300	17 AAR99959	B. t. coleopteran
53	271	42.1	914	12 AAR15785	B. thuringiensis to
54	220	34.2	644	22 AAB84195	Amino acid sequenc
55	67	10.4	67	23 AAW81937	Bacillus thuringie
56	67	10.4	80	16 AAR85484	Blt synthetic crys
57	66	10.2	68	16 AAR85483	Blt crystal proteol
58	54	8.4	54	23 AAW81938	Bacillus thuringie
59	38	5.9	38	23 AAW81939	Bacillus thuringie
60	36	5.6	36	23 AAW81940	Bacillus thuringie
61	35	5.4	35	23 AAW81941	Bacillus thuringie
62	33	5.1	33	23 AAW81942	Bacillus thuringie
63	31	4.8	31	23 AAW81943	Bacillus thuringie
64	30	4.7	30	23 AAW81944	Bacillus thuringie
65	29	4.7	30	23 AAW81945	Bacillus thuringie
66	29	4.5	29	23 AAW81946	Bacillus thuringie
67	28	4.3	28	23 AAW81947	Bacillus thuringie
68	28	4.3	28	23 AAW81948	Bacillus thuringie
69	28	4.3	28	23 AAW81949	Bacillus thuringie
70	28	4.3	28	23 AAW81950	Bacillus thuringie
71	28	4.3	28	23 AAW81951	Bacillus thuringie
72	27	4.2	27	23 AAW81952	Bacillus thuringie
73	27	4.0	26	23 AAW81953	Bacillus thuringie
74	25	3.9	25	23 AAW81954	Bacillus thuringie
75	25	3.9	25	23 AAW81955	Bacillus thuringie
76	24	3.7	24	20 AAY23201	Amino acid sequenc
77	24	3.7	24	20 AAY23202	Amino acid sequenc
78	24	3.7	24	20 AAY23203	Amino acid sequenc
79	24	3.7	24	20 AAY23204	Amino acid sequenc
80	24	3.7	24	20 AAY23205	Amino acid sequenc
81	24	3.7	24	20 AAY23206	Amino acid sequenc
82	23	3.6	23	12 AAW70445	Bacillus thuringie
83	23	3.6	23	12 AAW70446	Bacillus thuringie
					Blt109P Insecticid

Amino acid sequence
Bacillus thuringiensis
Bacillus thuringiensis
Amino acid sequence
Sequence encoded by
BtGst1208 protoxin
Bt isolate 43F. B
Antiscarab pest
Amino acid sequence
Amino acid sequence
B. thuringiensis Cr
Amino acid sequence
Amino acid sequence
Amino acid sequence
Amino acid sequence
Amino acid sequence
Amino acid sequence

ALIGNMENTS

RESULT 1
AAP70085
ID AAP70085 standard; Protein; 644 AA.
vv

AAP70085;

04-MAY-1991 (first entry)

DE Sequence of toxin which is toxic to beetles of the order
DE Coleoptera.

KW Microbial pesticide

Bacillus thuringiensis strain san diego

PN EP213818-A.

PD 11-MAR-1987

PF 08-AUG-1986; 86EP-0306151.

PR 16-JUN-1986; 86US-0874727.

XXXXXX

XX XX

[illegible]

DR N-PSDB; AAN70092

PT New poly:peptide toxin having pesticidal activity - formed by

PT Coleoptera beetles

PS Claim 3; pp15-16; 19pp; English.

B. thuringiensis toxin gene toxic to Coleoptera beetles is cloned

CC killing, the beetles are obtd. The polypeptide toxin may be isolated

[illegible]

Query Match	100.0%	Score 644;	DB 8;	Length 644;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 644;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 MNPNNRSEHDTIKTTENNEVPTHVQYPLAETPNPPTLEDLNYKEFLRMATADNNTAALDSS 600
|||||
1 MNPNNRSEHDTIKTTENNEVPTHVQYPLAETPNPPTLEDLNYKEFLRMATADNNTAALDSS 600

QY	61	TKKDVIQKIGISVWGBGLICVSGPFGGALVSYTYTNFLMTIMPSBDDPMKAFMEQVBEALMDOK	120
Db	61	TTKDVIOQIGISVWGBGLICVSGPFGGALVSYTYTNFLMTIMPSBDDPMKAFMEQVBEALMDOK	120
QY	121	IADYAKNKALAELOGLQNNVEDYYSALTSWQKNVSSRNHPSQGRIRELFSQAESHFRNS	180
Db	121	IADYAKNKALAELOGLQNNVEDYYSALTSWQKNVSSRNHPSQGRIRELFSQAESHFRNS	180
QY	181	MPSEFISGIEVULFTTYAQAAANTHLFLIKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT	240
Db	181	MPSEFISGIEVULFTTYAQAAANTHLFLIKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT	240
QY	241	DHCWYVWVNGDLKRGSSYESWVNFNRYRREMTLTJVDLIALPPLYDYRIKPREVTELT	300
Db	241	DHCWYVWVNGDLKRGSSYESWVNFNRYRREMTLTJVDLIALPPLYDYRIKPREVTELT	300
QY	301	RDVLTPDIYGVNNLRKGYGTTFSENIENTIRKPHLEFDYLAHIOFHTRFOPGYGNDSEFYMS	360
Db	301	RDVLTPDIYGVNNLRKGYGTTFSENIENTIRKPHLEFDYLAHIOFHTRFOPGYGNDSEFYMS	360
QY	361	GNVYSTPESIGSNDIITSPEFYGNKSSEPYONLEFNGEKYVRAVANTNLAVMPSAVYSGYT	420
Db	361	GNVYSTPESIGSNDIITSPEFYGNKSSEPYONLEFNGEKYVRAVANTNLAVMPSAVYSGYT	420
QY	421	KVESQYVNDQJDEASTQTYDSKRNVGAVSWDSIDOLPPEITDDEPLEKGYSHQJLNYMCEL	480
Db	421	KVESQYVNDQJDEASTQTYDSKRNVGAVSWDSIDOLPPEITDDEPLEKGYSHQJLNYMCEL	480
QY	481	MQGSKGTIPVLTJWTHKSYDFEFNMJDSKKITQLPYVKYKIKQSASVYAGRPFGGDIIOC	540
Db	481	MQGSKGTIPVLTJWTHKSYDFEFNMJDSKKITQLPYVKYKIKQSASVYAGRPFGGDIIOC	540
QY	541	TENGSAATIIYTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYFEDKTIINKGDTLT	600
Db	541	TENGSAATIIYTPDVYSQKYRARIHYASTSQITFTLSLDGAPFNQYFEDKTIINKGDTLT	600
QY	601	YNSFNJLASFTPEFLSGNNQIOGYTGJLSADCKYIYDKIEFTIPV	644
Db	601	YNSFNJLASFTPEFLSGNNQIOGYTGJLSADCKYIYDKIEFTIPV	644

RESULT 2

ID AAP82487 standard; protein; 644 AA.

AC AAP82487

DT 01-NOV-1990 (first entry)

DE Delta endotoxin encoded by cryc.

KW Coleoptera; toxin; cryc; insecticide; delta-endotoxin; Lepidoptera

OS *Bacillus thuringiensis* EG2158.

FH	Key	Location/Qualifiers
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100	100	100

/label=signal_peptide

FT	Protein	54..644
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Query Match	Best Local Similarity	100.0%	Score 644:	DB 9:	Length 644:	
Matches 644:	Conservative	0:	Mismatches	0:	Indels	Gaps
1	MNPNRSEHDITIKTTENNEVPTNHQVPLAETPNPTLEDLANKKEFLRMTADNNTALDSS	60				
1	MNPNRSEHDITIKTTENNEVPTNHQVPLAETPNPTLEDLANKKEFLRMTADNNTALDSS	60				
61	TTKDVIQGISVYGDLLGVYGFPGGALYSFTTNELNTWSPEDPKKAMEQVEALMDOK	120				
61	TTKDVIQGISVYGDLLGVYGFPGGALYSFTTNELNTWSPEDPKKAMEQVEALMDOK	120				
121	IADYKKNALAELOGIQQNVVEDYVSAISSMOKNPSSRRPHSGRIREFLSQAESHFRNS	180				
121	IADYKKNALAELOGIQQNVVEDYVSAISSMOKNPSSRRPHSGRIREFLSQAESHFRNS	180				
181	MPSFAISGEYVLEFLLTYAAOANTHLFLKDAOIYGEEMWYEKEDIAEFYKROLKLTQEXT	240				
181	MPSFAISGEYVLEFLLTYAAOANTHLFLKDAOIYGEEMWYEKEDIAEFYKROLKLTQEXT	240				
241	DHCVMYVNYNGDLKIGSSYSVSNVNFRRYREMTLVLDLIALFPLVDVRLYPREKYTELT	300				
241	DHCVMYVNYNGDLKIGSSYSVSNVNFRRYREMTLVLDLIALFPLVDVRLYPREKYTELT	300				
301	RDVLDPYIGVYNNLRGSGYGTTFSENIENYIRKPHLFYDLHRIOFHTRPQGYGNDSEFNYS	360				
301	RDVLDPYIGVYNNLRGSGYGTTFSENIENYIRKPHLFYDLHRIOFHTRPQGYGNDSEFNYS	360				
361	GNVYSTRPSIGSNDITTSFPGYKKSSEPVQNLFEENEKYYRAVANNNLAWPAAVYSGVY	420				
361	GNVYSTRPSIGSNDITTSFPGYKKSSEPVQNLFEENEKYYRAVANNNLAWPAAVYSGVY	420				
421	KVEFSQYNDQOTDEASQOTYDSKRNVAVSMDSIDQLPPTETDDEPLEKGYSHQNLVWCFL	480				
421	KVEFSQYNDQOTDEASQOTYDSKRNVAVSMDSIDQLPPTETDDEPLEKGYSHQNLVWCFL	480				
481	MOGSRGCTIEVLWTNHSYDFENMIDSKITQLPLVYAKYIKQSGASVYAGRFPFGDITOC	540				
481	MOGSRGCTIEVLWTNHSYDFENMIDSKITQLPLVYAKYIKQSGASVYAGRFPFGDITOC	540				
541	TENGSAATYVMPDVYSIQYRARIHASTSQTTLSTLDGAPFNQYFPKTIINKGDTLT	600				
541	TENGSAATYVMPDVYSIQYRARIHASTSQTTLSTLDGAPFNQYFPKTIINKGDTLT	600				
601	YNSFNLASFTPELSGNNLQIGVTGHSAGDKYIKIEEIPVYV	644				
601	YNSFNLASFTPELSGNNLQIGVTGHSAGDKYIKIEEIPVYV	644				

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OY 181 MSPFAISGVEVFLTTTAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
DB 181 MSPFAISGVEVFLTTTAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
OY 241 DHCVKMYNNGLDLGRSSYSWVNFNRYRREMTLVLDLALFPLYDRLYKREKTELT 300
DB 241 DHCVKMYNNGLDLGRSSYSWVNFNRYRREMTLVLDLALFPLYDRLYKREKTELT 300
OY 301 RDVLTDPPIGVNNLRGYSNENIENYIRKPHLFDVLRHQHTRFQPCYNDSPFNWS 360
DB 301 RDVLTDPPIGVNNLRGYSNENIENYIRKPHLFDVLRHQHTRFQPCYNDSPFNWS 360
OY 361 GNVYSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVYSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
OY 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
DB 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
OY 481 MOGSRGTIPVLVTHKSVDFNNIDSKKITQPLVKAAYKLGASAVVAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLVTHKSVDFNNIDSKKITQPLVKAAYKLGASAVVAGPRTGGDIIOC 540
OY 541 TENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
DB 541 TENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
OY 601 YNSFNLAFTSPFELSGNNLQIGVTLGASGDKVYIDKIEFIPVN 644
DB 601 YNSFNLAFTSPFELSGNNLQIGVTLGASGDKVYIDKIEFIPVN 644

RESULT 4
AAP95585
ID AAP95585 standard; protein: 644 AA.
AC AAP95585;
XX 08-AUG-1990 (first entry)
DE M-7 crystal toxin.
XX M-7 crystal toxin.
KW M-7 toxin crystal; Coleoptera: beetle.
OS Bacillus thuringiensis strain san-diego (NRRL B-15939).
PN US4853331-A.
PD 01-AUG-1989.
XX 30-NOV-1988; 88US-0278292.
PR 16-AUG-1985; 85US-0767227.
XX 15-JUL-1988; 88US-0219420.
PA (MICO-) MYCOGEN CORP.
XX Hernstadt C, Wilcox E;
PI WPI; 1989-277854/38.
XX DR N-PSDB; AAN90957.
XX N-PSDB; AAN90957.
XX Cloning of Bacillus thuringiensis toxin gene -
PT for expression of protein toxic to beetles of order Coleoptera.
XX Disclosure; Page 13-14; 10pp; English.
XX The gene encoding the toxin can be cloned and used to produce the
CC M-7 crystal which has activity against eg western spotted cucumber
XX beetle, and northern, western and southern corn rootworm.
SQ Sequence 644 AA;

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Query Match 100.0%; Score 644; DB 10; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNPNRSHDITKTENNEVPTNINVOYPLAETPPTLEDLNYKFEFLMTADNNTALDSS 60
DB 1 MNPNRSHDITKTENNEVPTNINVOYPLAETPPTLEDLNYKFEFLMTADNNTALDSS 60
OY 61 TTKDVIOKGISVVDLLGVVGFPEFGALVSEFYTLMTIMPSEDPKMAFEQYALMDOK 120
DB 61 TTKDVIOKGISVVDLLGVVGFPEFGALVSEFYTLMTIMPSEDPKMAFEQYALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDVYALSQKNPVSRRPHSGRIRELSQAESHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDVYALSQKNPVSRRPHSGRIRELSQAESHFRNS 180
OY 181 MSPFAISGVEVFLTTTAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
DB 181 MSPFAISGVEVFLTTTAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
OY 241 DHCVKMYNNGLDLGRSSYSWVNFNRYRREMTLVLDLALFPLYDRLYKREKTELT 300
DB 241 DHCVKMYNNGLDLGRSSYSWVNFNRYRREMTLVLDLALFPLYDRLYKREKTELT 300
OY 301 RDVLTDPPIGVNNLRGYSNENIENYIRKPHLFDVLRHQHTRFQPCYNDSPFNWS 360
DB 301 RDVLTDPPIGVNNLRGYSNENIENYIRKPHLFDVLRHQHTRFQPCYNDSPFNWS 360
OY 361 GNVYSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVYSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
OY 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
DB 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
OY 481 MOGSRGTIPVLVTHKSVDFNNIDSKKITQPLVKAAYKLGASAVVAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLVTHKSVDFNNIDSKKITQPLVKAAYKLGASAVVAGPRTGGDIIOC 540
OY 541 TENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
DB 541 TENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
OY 601 YNSFNLAFTSPFELSGNNLQIGVTLGASGDKVYIDKIEFIPVN 644
DB 601 YNSFNLAFTSPFELSGNNLQIGVTLGASGDKVYIDKIEFIPVN 644

RESULT 5
AAR39751
ID AAR39751 standard; protein: 644 AA.
AC AAR39751;
XX 28-JAN-1994 (first entry)
DE Delta endotoxin.
XX Endotoxin; Bacillus; lice; insecticide; sheep.
XX Bacillus thuringiensis PS40D1.
XX WO9314641-A.
XX 05-AUG-1993.
XX 31-DEC-1992; 92MO-US11337.
XX 29-JAN-1992; 92US-0828768.
XX (MICO ) MYCOGEN CORP.

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XX Hickie LA, Payne J;
 XX WPI: 1993-258266/32.
 DR N-PSDB: AAQ47288.
 XX
 PT Controlling biting lice on sheep - comprises administering
 PT Bacillus thuringiensis toxins to host
 PS
 XX Disclosure: Page 31-32; 64pp; English.
 CC Many strains of Bacillus thuringiensis (B.t.) produce insecticidal
 CC delta endotoxins. A number of these endotoxins have been found to
 CC be toxic to *Damillia* ovis, the biting louse of sheep. The B.T.
 CC isolates which produce these toxins can be grown and the delta
 CC endotoxin which is produced can be recovered by standard procedures.
 CC The genes encoding these endotoxins can also be transferred to a
 CC suitable host via a recombinant vector and the resulting
 CC transformants used in methods to control lice.
 XX
 XX Sequence 644 AA:
 SQ
 Query Match 100.0%; Score 644; DB 14; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
 DB 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
 QY 61 TTKDVYOKGISVVDLGLGVGPPFGALVSFTNTLNTIMPSEDPMKAFMEVEALMDOK 120
 DB 61 TTKDVYOKGISVVDLGLGVGPPFGALVSFTNTLNTIMPSEDPMKAFMEVEALMDOK 120
 QY 121 IDVANKKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSGRIREFLSQAESHPFNS 180
 DB 121 IDVANKKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSGRIREFLSQAESHPFNS 180
 QY 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKRQKLQET 240
 DB 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKRQKLQET 240
 QY 241 DHCVKWYNGDLKLRGSSYESWVNFRRREMTLYLDLALFPLDYRLVLPKEVKTET 300
 DB 241 DHCVKWYNGDLKLRGSSYESWVNFRRREMTLYLDLALFPLDYRLVLPKEVKTET 300
 QY 301 RDVLTDPYGVNMLRGYGTTFESIENYIRKPHLFYDLHRIQFHTRPQGYGNDSEFNWS 360
 DB 301 RDVLTDPYGVNMLRGYGTTFESIENYIRKPHLFYDLHRIQFHTRPQGYGNDSEFNWS 360
 QY 361 GNVYSTRPSIGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPAAVSGYT 420
 DB 361 GNVYSTRPSIGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPAAVSGYT 420
 QY 421 KVEFSQYNDQDEASTQTYDSKRNVAWSIDQLPETTDEPLEKGYSHQNLVWCF 480
 DB 421 KVEFSQYNDQDEASTQTYDSKRNVAWSIDQLPETTDEPLEKGYSHQNLVWCF 480
 QY 481 MGSRGCTPVLWTMHSKVDENFMIDSKKIKQLPLVKAQKQSGASVAVAGRFGDIIOC 540
 DB 481 MGSRGCTPVLWTMHSKVDENFMIDSKKIKQLPLVKAQKQSGASVAVAGRFGDIIOC 540
 QY 541 TENSSAATIVTTPVVSQYRARIHASTSQTFTLSLGGAPFNQYFPKTKINKGDTLT 600
 DB 541 TENSSAATIVTTPVVSQYRARIHASTSQTFTLSLGGAPFNQYFPKTKINKGDTLT 600
 QY 601 YNSFNLASFTPELSCGNLQIGVTLGASDKVYIDKIEEIPVN 644
 DB 601 YNSFNLASFTPELSCGNLQIGVTLGASDKVYIDKIEEIPVN 644

ID AAR56697 standard; Protein; 644 AA.
 XX
 XX AAR56697;
 AC
 XX 27-MAR-1995 (first entry)
 DT
 XX
 DE CryIIIA insecticidal crystal protein.
 XX
 KW CryIIIA; CryIIIA; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;
 KW Lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
 KW probe; hybridisation.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US5338544-A.
 XX
 PD 16-AUG-1994.
 XX
 PF 16-APR-1987; 87US-0039542.
 XX
 PR 16-APR-1987; 87US-0039542.
 PR 11-JUL-1989; 89US-0379015.
 PR 28-AUG-1991; 91US-0751452.
 PR 26-FEB-1993; 93US-0023736.
 XX
 PA (ECOG-) ECOGEN INC.
 PI Donovan WP;
 XX
 XX WPI: 1994-263236/32.
 DR N-PSDB: AAQ71026.
 XX
 PT New Cry IIB protein - obtd. from the cry II B gene in Bacillus
 PT thuringiensis var. kurstaki, active against lepidopteran insects
 XX
 PS Example 7; Fig 4A-4D; 39pp; English.
 XX
 CC This sequence shows the amino acid sequence of CryIIIA protein. The
 CC promoter from the CryIIIA gene sequence was fused to the protein
 CC coding region of the CryBI gene (AAQ71027). The recombinant hybrid
 CC fusion gene expressed the CryBI crystal protein more efficiently
 CC than its native promoter. CryIIB encodes an insecticidal crystal
 CC protein isolated from Bacillus thuringiensis var. kurstaki. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. Lepidoptera.
 CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR56696 and AAR56698)
 XX
 XX Sequence 644 AA:
 SQ
 Query Match 100.0%; Score 644; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
 DB 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
 QY 61 TTKDVYOKGISVVDLGLGVGPPFGALVSFTNTLNTIMPSEDPMKAFMEVEALMDOK 120
 DB 61 TTKDVYOKGISVVDLGLGVGPPFGALVSFTNTLNTIMPSEDPMKAFMEVEALMDOK 120
 QY 121 IDVANKKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSGRIREFLSQAESHPFNS 180
 DB 121 IDVANKKALAELOGLQNNVEDYVSALSSWQKNPVSSRRPHSGRIREFLSQAESHPFNS 180
 QY 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKRQKLQET 240
 DB 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKRQKLQET 240
 QY 241 DHCVKWYNGDLKLRGSSYESWVNFRRREMTLYLDLALFPLDYRLVLPKEVKTET 300
 DB 241 DHCVKWYNGDLKLRGSSYESWVNFRRREMTLYLDLALFPLDYRLVLPKEVKTET 300

QY 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 CC 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 CC 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 Db 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 QY 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPMSAVYSGVT 420
 Db 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPMSAVYSGVT 420
 QY 421 KVEFSQYNDOTDEASTQYTDKRNKAVSWDSIDQLPETTDEPLEKGYSHOINVMCF 480
 Db 421 KVEFSQYNDOTDEASTQYTDKRNKAVSWDSIDQLPETTDEPLEKGYSHOINVMCF 480
 QY 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVAKYLGASGVAGPRTGGDIIOC 540
 Db 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVAKYLGASGVAGPRTGGDIIOC 540
 QY 541 TENGSAATYIVTPDVSYSKYRARIHYASTSQITFTLSDGAPFNQYFDDTKINKGDTLT 600
 Db 541 TENGSAATYIVTPDVSYSKYRARIHYASTSQITFTLSDGAPFNQYFDDTKINKGDTLT 600
 QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644
 Db 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644

RESULT 7
 AAR56698
 ID AAR56698 standard; Protein: 644 AA.

AC AAR56698;

DT 27-MAR-1995 (first entry)

DE CryIIB insecticidal crystal protein.

KW CryIIA, CryIIIA, CryIIB, CryC, P-2; CryBI; insecticidal protein crystal;
 KX Lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
 KW probe; hybridisation.

OS Bacillus thuringiensis.

XX US5338544-A.

XX 16-AUG-1994.

XX 16-APR-1987; 87US-0039542.

XX 16-APR-1987; 87US-0039542.

XX 11-JUL-1989; 89US-0379015.

XX 28-AUG-1991; 91US-0751452.

XX 26-FEB-1993; 93US-0023736.

XX (ECOCG-) ECOGEN INC.

XX Donovan WP;

XX WPI; 1994-263236/32.

XX N-PSDB; AAQ71027.

XX New Cry IIB protein - obt'd. from the cry II B gene in Bacillus
 thuringiensis var. kurstaki, active against lepidopteran insects

XX Claim 1; Fig 6A-6D; 39pp; English.

CC This sequence shows the amino acid sequence of CryIIB protein. The
 CC promoter from the CryIIA gene (AAQ71026) sequence was fused to the
 CC protein coding region of the CryIIB gene. The recombinant hybrid
 CC fusion gene expressed the CryIIB crystal protein more efficiently
 CC than its native promoter. CryIIB encodes an insecticidal crystal
 CC protein isolated from Bacillus thuringiensis var. kurstaki. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. lepidopterans.

CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR56696 and AAR56698)

XX Sequence 644 AA;

Query Match 100.0%; Score 644; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVEPTNHVQYPLAETPPTLEDINYEKFLBMTADNNTAEDSS 60
 Db 1 MNPNNRSEHDITKTENNENVEPTNHVQYPLAETPPTLEDINYEKFLBMTADNNTAEDSS 60
 QY 61 TTKDVYQKGISVGDLLGVGFPFGALVSEFYNNFLMTIMPSDDPWKAEQYBALMDQK 120
 Db 61 TTKDVYQKGISVGDLLGVGFPFGALVSEFYNNFLMTIMPSDDPWKAEQYBALMDQK 120
 QY 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSRNPHSGRTRELFSQASHFRNS 180
 Db 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSRNPHSGRTRELFSQASHFRNS 180
 QY 181 MPSEFAISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROKLTOEYV 240
 Db 181 MPSEFAISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROKLTOEYV 240
 QY 241 DHCYKMYNNGLDKRGSSYSESVNFRNRYRREMTLTVLDLALPLDYRYPREVTELT 300
 Db 241 DHCYKMYNNGLDKRGSSYSESVNFRNRYRREMTLTVLDLALPLDYRYPREVTELT 300
 QY 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 Db 301 RDVLTDPVGVNRLRGYGTTFSENIEYIRKPHLFDYLRHIOFHTRRPOGYGNDSPFNYS 360
 QY 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPMSAVYSGVT 420
 Db 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPMSAVYSGVT 420
 QY 421 KVEFSQYNDOTDEASTQYTDKRNKAVSWDSIDQLPETTDEPLEKGYSHOINVMCF 480
 Db 421 KVEFSQYNDOTDEASTQYTDKRNKAVSWDSIDQLPETTDEPLEKGYSHOINVMCF 480
 QY 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVAKYLGASGVAGPRTGGDIIOC 540
 Db 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVAKYLGASGVAGPRTGGDIIOC 540
 QY 541 TENGSAATYIVTPDVSYSKYRARIHYASTSQITFTLSDGAPFNQYFDDTKINKGDTLT 600
 Db 541 TENGSAATYIVTPDVSYSKYRARIHYASTSQITFTLSDGAPFNQYFDDTKINKGDTLT 600
 QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644
 Db 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644

RESULT 8
 AAY23214
 ID AAY23214 standard; Protein: 652 AA.

AC AAY23214;

DT 24-AUG-1999 (first entry)

DE Amino acid sequence of Cry3A protein.

XX Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
 KW Coleoptera; southern corn rootworm; western corn root worm; Cry3A;
 KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
 KW Diabrotica virgifera virgifera Leconte; insecticide resistance.

OS Bacillus thuringiensis.

XX W09931248-A1.

PD 24-JUN-1999.
 XX 17-DEC-1998; 98WO-US#6852.
 XX 18-DEC-1997; 97US-0996441.
 PR 18-DEC-1997; 97US-0993170.
 PR 18-DEC-1997; 97US-0993722.
 PR 18-DEC-1997; 97US-0993775.
 XX (ECOG-) ECOGEN INC.
 PA (MONS) MONSANTO CO.
 XX Brunsack SM, Bryson JW, English L, Kulesza CA, Malvar TM;
 PI Romano C, Staltin SL, Von Tersch MA, Walters FS;
 XX WPI: 1999-395184/33.
 DR Insecticidal *Bacillus thuringiensis* proteins
 XX
 PT Disclosure: Page 505-507; 512pp; English.
 XX
 PS The present sequence represents the Cry3A protein. The specification
 CC describes new *Bacillus thuringiensis* Cry3Bb mutant proteins, and
 CC provides methods for producing them. The B. thuringiensis Cry3Bb
 CC polypeptide was modified to have improved insecticidal activity or
 CC enhanced insecticidal specificity against a target insect. The
 CC modification comprises at least one amino acid substitution, addition,
 CC or deletion in the primary sequence of the native or unmodified Cry3Bb
 CC polypeptide, wherein the substitution or deletion occurs at a position
 CC corresponding to from about amino acids 1-365 of the unmodified
 CC polypeptide sequence (AAV23207 represents the wild type Cry3Bb
 CC protein). The polypeptide can be used to kill coleopteran pests,
 CC especially by application to the environment. It is especially
 CC useful against southern corn rootworm and western corn root worm,
 CC (*Diabrotica undecimpunctata howardi* Barber, and *Diabrotica virgifera*
 CC *vergifera* Lecoute respectively). The mutant cry3Bb polynucleotides
 CC can also be used to produce transgenic plants with increased
 CC insecticide resistance.
 CC
 XX Sequence 652 AA:
 SQ
 Query Match 100.0%; Score 644; DB 20; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 KVERSOYNDOTDEASTOTYDSCRNVGAVSWDSIDOLPPTETDDELEKGYSHQUNYMCFL 480
 |||||||
 DB 429 KVERSOYNDOTDEASTOTYDSCRNVGAVSWDSIDOLPPTETDDELEKGYSHQUNYMCFL 488
 OY 481 MOGSRGTIPVLWTMHSVDFEENMIDSKITQPLVKAAYKQSGASVAVGPRFTGDIIOC 540
 DB 489 MOGSRGTIPVLWTMHSVDFEENMIDSKITQPLVKAAYKQSGASVAVGPRFTGDIIOC 548
 OY 541 TENGAATITVTPDVSTQKRYRARIHASTQITFTLSLDGAFPNQYFPDKTINKGDTLT 600
 |||||||
 DB 549 TENGAATITVTPDVSTQKRYRARIHASTQITFTLSLDGAFPNQYFPDKTINKGDTLT 608
 OY 601 YNSFNLASFPPELSCNNLOIGVTGLSAGDKYIDKIEFIPVN 644
 |||||||
 DB 609 YNSFNLASFPPELSCNNLOIGVTGLSAGDKYIDKIEFIPVN 652

RESULT 9
 AAM00334
 ID AAM00334 standard; Protein: 597 AA.
 XX
 AC AAM00334;
 XX
 DT 02-JAN-1997 (first entry)
 XX
 DE *Bacillus thuringiensis* pesticidal protein toxin (native).
 XX
 KW *Bacillus thuringiensis*; plant; codon; crystal protein; Bt gene;
 XX toxin; insect; pest; tobacco hornworm.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN US5567600-A.
 XX
 PD 22-OCT-1996.
 XX
 PF 24-SEP-1983; 83US-0535354.
 XX
 PR 06-JAN-1995; 95US-0369835.
 PR 24-SEP-1983; 83US-0535354.
 PR 04-APR-1986; 86US-0848733.
 PR 09-SEP-1988; 88US-0242482.
 PR 28-JAN-1992; 92US-0827844.
 PR 03-MAY-1993; 93US-0057191.
 XX
 XX (MYCO) MYCOGEN PLANT SCI INC.
 XX
 PA Adang MJ, Merlo DJ, Murray EE, Rochelleau JA;
 PI
 XX WPI: 1996-484994/48.
 DR N-PSDB: AAT40341.
 XX
 PT Increasing *Bacillus thuringiensis* gene expression in plants - by
 PS reducing frequency of codon usages that are rare in plants
 XX
 PS Disclosure: Fig 1; 23pp; English.
 XX
 CC The synthetic Bt gene sequence (AAT40340) differs from the native
 CC sequence as found in p344pst-Met5 (AAT40341). Changes in amino acids
 CC occur in the synthetic sequence with alanine replacing threonine at
 CC residue 2 and leucine replacing the stop at residue 596 followed by
 CC the addition of 13 amino acids at the C-terminus.
 CC At least 32% of the codons and/or at least 11% of the nucleotides
 CC in the coding sequence of the native Bt gene are changed.
 CC By avoiding codon usage that are rare in plants, plants that have
 CC more Bt crystal protein than plants contg. the native Bt gene, and
 CC are thus more toxic to insect pests such as tobacco hornworm, can be
 CC produced.
 XX
 SQ Sequence 597 AA;
 Query Match 92.7%; Score 597; DB 17; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 597: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 48 MTADNNTALDSSTTKDVIOKGISVVDLIGVGFPGGALVSFYTNFLTWTWPSDEPK 107
DB 1 MTADNNTALDSSTTKDVIOKGISVVDLIGVGFPGGALVSFYTNFLTWTWPSDEPK 60
OY 108 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNHSGGRIR 167
DB 61 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNHSGGRIR 120
OY 168 ELFSQAESHRNSMPSFAISGEVFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAD 227
DB 121 ELFSQAESHRNSMPSFAISGEVFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAD 180
OY 228 FYKROLKLTQETDHCVKYNNVGLDKLRGSSYESVWNNFRYRREMTLVLDLIALPPLYD 287
DB 181 FYKROLKLTQETDHCVKYNNVGLDKLRGSSYESVWNNFRYRREMTLVLDLIALPPLYD 240
OY 288 VRLYPEVKTETLRDVLDPDPIGVNNLRGVTTSNIENYIRKPHLFDYLHRIQFHTRRQ 347
DB 241 VRLYPEVKTETLRDVLDPDPIGVNNLRGVTTSNIENYIRKPHLFDYLHRIQFHTRRQ 300
OY 348 PGYYGNDSEFNYSNGVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTN 407
DB 301 PGYYGNDSEFNYSNGVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTN 360
OY 408 LAWPSAVYSGVTKEFQSYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 467
DB 361 LAWPSAVYSGVTKEFQSYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 420
OY 468 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKKITQPLVAKYKLOGSASV 527
DB 421 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKKITQPLVAKYKLOGSASV 480
OY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITFTLSIDGAPFNQY 587
DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITFTLSIDGAPFNQY 540
OY 588 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 541 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

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RESULT 10
AAV69666 standard: Protein: 597 AA.

AC AAV69666:
XX
XX 08-MAY-2000 (first entry)
XX
XX Wild-type *Bacillus thuringiensis* (Bt) toxin.
XX
XX Bt toxin: codon usage; expression: transgenic plant; pesticide.
XX
XX insecticide.
OS *Bacillus thuringiensis* var. *tenebrionis*.
XX
XX US6015891-A.
XX
XX 18-JAN-2000.
XX
XX 29-AUG-1996; 9605-0705438.
XX
XX 06-JAN-1995; 9505-0369835.
XX 09-SEP-1988; 8805-0242482.
XX 28-JAN-1992; 9205-0827844.
XX 03-MAY-1993; 9305-0057191.
PA (MYCO) MYCOGEN PLANT SCI INC.
XX
XX Murray EE, Adang MJ;
XX

DR WPI: 2000-136460/12.
DR N-PSDB: AA259993.
XX
XX Synthetic *Bacillus thuringiensis* pesticidal toxin gene for expression
PT in plant cells has coding sequence adapted to codon usage bias of
PT plants.
XX
XX Example 3: Columns 31-36; 29pp; English.
XX
XX The invention relates to a novel synthetic *Bacillus thuringiensis* (Bt)
CC toxin gene (AA259994) which is expressed at a high level in descendant
CC plant cells and encodes a pesticidal protein toxin. The synthetic gene
CC was designed to be expressed in plants at a higher level than wild-type
CC Bt genes (e.g., AA259993). This was accomplished by altering the DNA
CC sequence of the native Bt gene such that it contained codons
CC preferred by highly expressed plant genes, had an A+T content comparable
CC to that found in plant genes and contained a plant initiation sequence.
CC Additionally, sequences that cause destabilization, inappropriate
CC polyadenylation, degradation and termination of RNA were eliminated,
CC and sequences that constitute RNA hairpin and splice sites were avoided.
CC The resulting synthetic Bt gene has at least 10% of its nucleotides
CC altered as compared with the native Bt gene. The synthetic Bt gene is
CC operably linked to a plant-expressible promoter and can be transformed
CC into plant cells. The gene is used to produce transgenic plants having
CC resistance to pests, particularly insects. The modifications produced in
CC the coding sequence increases the level of expression of Bt toxin in
CC plants. The present sequence represents wild-type *Bacillus thuringiensis*
CC (var. *tenebrionis*, Btt) Bt toxin.
XX
XX Sequence 597 AA:
SQ
Query Match 92.7%; Score 597; DB 21; Length 597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 48 MTADNNTALDSSTTKDVIOKGISVVDLIGVGFPGGALVSFYTNFLTWTWPSDEPK 107
DB 1 MTADNNTALDSSTTKDVIOKGISVVDLIGVGFPGGALVSFYTNFLTWTWPSDEPK 60
OY 108 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNHSGGRIR 167
DB 61 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNHSGGRIR 120
OY 168 ELFSQAESHRNSMPSFAISGEVFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAD 227
DB 121 ELFSQAESHRNSMPSFAISGEVFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAD 180
OY 228 FYKROLKLTQETDHCVKYNNVGLDKLRGSSYESVWNNFRYRREMTLVLDLIALPPLYD 287
DB 181 FYKROLKLTQETDHCVKYNNVGLDKLRGSSYESVWNNFRYRREMTLVLDLIALPPLYD 240
OY 288 VRLYPEVKTETLRDVLDPDPIGVNNLRGVTTSNIENYIRKPHLFDYLHRIQFHTRRQ 347
DB 241 VRLYPEVKTETLRDVLDPDPIGVNNLRGVTTSNIENYIRKPHLFDYLHRIQFHTRRQ 300
OY 348 PGYYGNDSEFNYSNGVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTN 407
DB 301 PGYYGNDSEFNYSNGVSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTN 360
OY 408 LAWPSAVYSGVTKEFQSYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 467
DB 361 LAWPSAVYSGVTKEFQSYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 420
OY 468 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKKITQPLVAKYKLOGSASV 527
DB 421 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKKITQPLVAKYKLOGSASV 480
OY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITFTLSIDGAPFNQY 587
DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITFTLSIDGAPFNQY 540
OY 588 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 541 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

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Db 541 YFDKTKNGDITLYNSFNLSASTPFEELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

RESULT 11

AA05537

ID AAR05537 standard; protein: 610 AA.

AC AAR05537;

XX 02-AUG-1990 (first entry)

XX Synthetic Bacillus thuringiensis toxin.

XX Btl. toxin: insecticide; crystal protein.

XX Synthetic.

XX EP359472-A.

XX 21-MAR-1990.

XX 07-SEP-1989; 89EP-0309069.

XX 09-SEP-1988; 88US-0242482.

XX (LUBR) LUBRIZOL GENETICS.

XX Adang MJ, Rocheleau TA, Merlo DJ, Murray EE;

XX WPI: 1990-085243/12.

XX N-PSDB: AA003587.

XX Synthetic insecticidal crystal protein gene - comprises DNA sequence encoding insecticidal protein functionally equiv. to bacillus thuringiensis (Bt) insecticidal protein.

XX Disclosure; ; p: English.

XX The sequence is that of an insecticidal protein functionally equivalent to a native Bt protein. Plant cells expressing the protein have protection against insect damage. Differences between this sequence and that of the wild type comprise the replacement of Thr(2) and Stop(596) with Ala and Leu resp. and the addn. of 13 AAs to the C-terminus.

XX Sequence 610 AA;

Query Match 92.4%; Score 595; DB 11; Length 610;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSTTKDVIQKISVVGDLGIVYGFPGALVSEYTNFINTIMPSEDPKAF 109

DB 3 ADNNTALDSSTTKDVIQKISVVGDLGIVYGFPGALVSEYTNFINTIMPSEDPKAF 62

QY 110 MEQVEALMDOKIADYAKNKALAEIQIQQNNVEDYVSLSSMOKNPVSSRNPHSOGRIREL 169

DB 63 MEQVEALMDOKIADYAKNKALAEIQIQQNNVEDYVSLSSMOKNPVSSRNPHSOGRIREL 122

QY 170 FSOQSHFRNMPSEAFISGVEVLFITTYAQAANHLFLDLDAQIYGEEMKYEKEDIAEFY 229

DB 123 FSOQSHFRNMPSEAFISGVEVLFITTYAQAANHLFLDLDAQIYGEEMKYEKEDIAEFY 182

QY 230 KROKLTQEVYTHCVMKYNVGLDLKRGSSYESWVNFNRIRREMTLYLDLIALFPLDYVR 289

DB 183 KROKLTQEVYTHCVMKYNVGLDLKRGSSYESWVNFNRIRREMTLYLDLIALFPLDYVR 242

QY 290 LYREVEVTELTROVLDPIYGVNNLRGYGTFSNIENYIKKPHLFDYLRHQFHTPRQPG 349

DB 243 LYREVEVTELTROVLDPIYGVNNLRGYGTFSNIENYIKKPHLFDYLRHQFHTPRQPG 302

QY 350 YYGNDSEFNYSNGVYSTRPSIGSNDITSPYGNKSSSEPONLEFNEKYYRAVANNTLA 409

DB 303 YYGNDSEFNYSNGVYSTRPSIGSNDITSPYGNKSSSEPONLEFNEKYYRAVANNTLA 362

QY 410 VWPASVSGVTKVEFSGYNDQTEASTQYTDSCRNVGANSWDSIDOLPETTDEPLEKGY 469

DB 363 VWPASVSGVTKVEFSGYNDQTEASTQYTDSCRNVGANSWDSIDOLPETTDEPLEKGY 422

QY 470 SHOLNTVMCFLMOGSNGRTIPVLTMTHKSYDFEFMINDSKRTLOPLKAVKLGSGASVAG 529

DB 423 SHOLNTVMCFLMOGSNGRTIPVLTMTHKSYDFEFMINDSKRTLOPLKAVKLGSGASVAG 482

QY 530 PRFTGGDIIOCTENGSAATITVTPDVYSQKRYRARIHYASTSQITPFLSDGAPFNQYF 589

DB 483 PRFTGGDIIOCTENGSAATITVTPDVYSQKRYRARIHYASTSQITPFLSDGAPFNQYF 542

QY 590 DKTIKNGDITLYNSFNLSASTPFEELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

DB 543 DKTIKNGDITLYNSFNLSASTPFEELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

RESULT 12

AA00333

ID AAM00333 standard; protein: 610 AA.

AC AAM00333;

XX 02-JAN-1997 (first entry)

XX Bacillus thuringiensis pesticidal protein toxin (synthetic).

XX Bacillus thuringiensis; plant; codon: crystal protein; Btl gene;

XX toxin: insect; pest; tobacco hornworm.

XX Bacillus thuringiensis.

XX US5567600-A.

XX 22-OCT-1996.

XX 24-SEP-1983; 83US-0535354.

XX 06-JAN-1995; 95US-0369835.

XX 24-SEP-1983; 83US-0535354.

XX 04-APR-1986; 86US-0848733.

XX 09-SEP-1988; 88US-0242482.

XX 28-JAN-1992; 92US-0827844.

XX 03-MAY-1993; 93US-0057191.

XX (MYCO) MYCOGEN PLANT SCI INC.

XX Adang MJ, Merlo DJ, Murray EE, Rocheleau TA;

XX WPI: 1996-484994/48.

XX N-PSDB: AAT40340.

XX Increasing Bacillus thuringiensis gene expression in plants - by reducing frequency of codon usages that are rare in plants

XX Disclosure; Fig 1; 23pp; English.

XX The synthetic Btl gene sequence (AAT40340) differs from the native CC sequence as found in p544Pst-Met5 (AAT40341). Changes in amino acids CC occur in the synthetic sequence with alanine replacing threonine at CC residue 2 and leucine replacing the stop at residue 596 followed by CC the addition of 13 amino acids at the C-terminus.

XX At least 32% of the codons and/or at least 11% of the nucleotides CC in the coding sequence of the native Btl gene are changed.

XX By avoiding codon usage that are rare in plants, plants that have CC more Btl crystal protein than plants contg. the native Btl gene, and CC are thus more toxic to insect pests such as tobacco hornworm, can be CC produced.

XX Sequence 610 AA;

Query Match 92.4%; Score 595; DB 17; Length 610;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNTEALDSSSTTKDVIQKGISVGGDLGCVGFPGGALVSFYTNFLNTIMPSEDPKAKF 109
DB 3 ADNTEALDSSSTTKDVIQKGISVGGDLGCVGFPGGALVSFYTNFLNTIMPSEDPKAKF 62
QY 110 MEQVEALMDOOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 169
DB 63 MEQVEALMDOOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 122
QY 170 FSOAESHFNRNMPSPFAISGEVLEFLTTYQAANTHLFLKDAQIYGEEMGEKEEDIAEFY 229
DB 123 FSOAESHFNRNMPSPFAISGEVLEFLTTYQAANTHLFLKDAQIYGEEMGEKEEDIAEFY 182
QY 230 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRREMTLTVDLIALFPLYDVR 289
DB 183 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRREMTLTVDLIALFPLYDVR 242
QY 290 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNIENTYRKPHLFDYLHRIQFTRFOPG 349
DB 243 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNIENTYRKPHLFDYLHRIQFTRFOPG 302
QY 350 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKERYRAVANTNLA 409
DB 303 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKERYRAVANTNLA 362
QY 410 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 469
DB 363 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 422
QY 470 SHOLNVWCFILOGSGRGITPVLTWTHKSVDFNMIDSKKITDPLVAKKILQSGASVYAG 529
DB 423 SHOLNVWCFILOGSGRGITPVLTWTHKSVDFNMIDSKKITDPLVAKKILQSGASVYAG 482
QY 530 PRFTGGDIIQCTENGSAATITVTPDVYSQKYRARIHASTQITFTLSLDGAPFNQYIF 589
DB 483 PRFTGGDIIQCTENGSAATITVTPDVYSQKYRARIHASTQITFTLSLDGAPFNQYIF 542
QY 590 DKTINKGDTLTYSFNFLASFSTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 543 DKTINKGDTLTYSFNFLASFSTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 597

RESULT 13
AAI69667 standard; Protein; 610 AA.
ID AAI69667
AC AAI69667
XX
DT 08-MAY-2000 (first entry)
XX
DE *Bacillus thuringiensis* (Bt) toxin encoded by synthetic Bt gene.
XX
KW Bt toxin; codon usage; expression; transgenic plant; pesticide;
KM insecticide; mutant; mutcin.
XX
OS *Bacillus thuringiensis* var. *tenebrionis*.
OS Synthetic.
XX
PN US6015891-A.
XX
PD 18-JAN-2000.
XX
PF 29-AUG-1996; 96US-0705438.
XX
PR 06-JAN-1995; 95US-0369835.
PR 09-SEP-1988; 88US-0242482.
PR 28-JAN-1992; 92US-0827844.
PR 03-MAY-1993; 93US-0057191.
XX
PA (MYCO) MYCOGEN PLANT SCI INC.
XX

PI Murray EE, Adang MJ;
XX WPI, 2000-136460/12.
DR N-PSDB; AAI69667.
XX
PT Synthetic *Bacillus thuringiensis* pesticidal toxin gene for expression
in plant cells has coding sequence adapted to codon usage bias of
plants -
XX
XX
PS Example 3; Fig 1A-C; 29pp; English.
XX

This sequence represents a *Bacillus thuringiensis* (Bt) toxin encoded by a synthetic Bt gene (AAI69667). This gene is expressed at a high level in descendant plant cells and encodes a pesticidal protein toxin. The synthetic gene was designed to be expressed in plants at a higher level than wild-type Bt genes (e.g., AAI59993). This was accomplished by altering the DNA sequence of the native Bt gene such that it contained codons preferred by highly expressed plant genes, had an A+T content comparable to that found in plant genes and contained a plant initiation sequence. Additionally, sequences that cause destabilization, inappropriate polyadenylation, degradation and termination of RNA were eliminated, and sequences that constitute RNA hairpin and splice sites were avoided. The resulting synthetic Bt gene has at least 10% of its nucleotides altered as compared with the native Bt gene. The synthetic Bt gene is operably linked to a plant-expressible promoter and can be transformed into plant cells. The gene is used to produce transgenic plants having resistance to pests, particularly insects. The modifications produced in the coding sequence increases the level of expression of Bt toxin in plants.

Sequence 610 AA:

Query Match 92.4%; Score 595; DB 21; Length 610;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNTEALDSSSTTKDVIQKGISVGGDLGCVGFPGGALVSFYTNFLNTIMPSEDPKAKF 109
DB 3 ADNTEALDSSSTTKDVIQKGISVGGDLGCVGFPGGALVSFYTNFLNTIMPSEDPKAKF 62
QY 110 MEQVEALMDOOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 169
DB 63 MEQVEALMDOOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 122
QY 170 FSOAESHFNRNMPSPFAISGEVLEFLTTYQAANTHLFLKDAQIYGEEMGEKEEDIAEFY 229
DB 123 FSOAESHFNRNMPSPFAISGEVLEFLTTYQAANTHLFLKDAQIYGEEMGEKEEDIAEFY 182
QY 230 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRREMTLTVDLIALFPLYDVR 289
DB 183 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRREMTLTVDLIALFPLYDVR 242
QY 290 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNIENTYRKPHLFDYLHRIQFTRFOPG 349
DB 243 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNIENTYRKPHLFDYLHRIQFTRFOPG 302
QY 350 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKERYRAVANTNLA 409
DB 303 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKERYRAVANTNLA 362
QY 410 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 469
DB 363 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 422
QY 470 SHOLNVWCFILOGSGRGITPVLTWTHKSVDFNMIDSKKITDPLVAKKILQSGASVYAG 529
DB 423 SHOLNVWCFILOGSGRGITPVLTWTHKSVDFNMIDSKKITDPLVAKKILQSGASVYAG 482
QY 530 PRFTGGDIIQCTENGSAATITVTPDVYSQKYRARIHASTQITFTLSLDGAPFNQYIF 589
DB 483 PRFTGGDIIQCTENGSAATITVTPDVYSQKYRARIHASTQITFTLSLDGAPFNQYIF 542
QY 590 DKTINKGDTLTYSFNFLASFSTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

DB 543 DKTINKGDTLYNSFNFLASFSTPELSCNNLQIGVTGLSAGDKYIDKIEPTPVN 597

|||||

RESULT 14

AA015784 standard; Protein: 956 AA.

AA015784:

10-FEB-1992 (first entry)

B. thuringiensis toxin/AcNPV gp64 fusion protein.

chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae; midgut targeting; bacterial endotoxin; pfx7.

Bacillus thuringiensis var. tenebriosis.

Autographa californica Nuclear Polyhedrosis Virus.

MO9117254-A.

14-NOV-1991.

02-MAY-1991: 91WO-US03008.

03-MAY-1990: 90US-0518575.

(REGC) UNIV OF CALIFORNIA.

Sivasubramanian N, Federici A;

WPI: 1991-353775/48.

N-PSDB: AA014806.

Extending host range or toxicity of insecticidal proteins - using protein capable of binding to gut epithelium of insects

Claim 55; Fig 17; 61pp; English.

A polylinker was inserted into the XmnI restriction site at the carboxyl terminus coding region of B. thuringiensis var. tenebriosis (Bt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV was operably linked to the Bt toxin coding sequence via the polylinker. The gp64 gene sequences act as midgut targeting signals for bacterial endotoxins. Plasmid pFX7 was one of three different Bt/gp64 gene fusions that were constructed and its deduced amino acid sequence is given here.

See also AA014806 and AA014808.

Sequence 956 AA:

Query Match 91.6%; Score 590; DB 12; Length 956;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 50 ANNNTEALDSSSTTKVIOKIGISVGDGLGVGFPFGALVSYTYTNFLMTWPSDEPKAF 109

16 ANNNTEALDSSSTTKVIOKIGISVGDGLGVGFPFGALVSYTYTNFLMTWPSDEPKAF 75

DB 110 MEQVEALMDOKIADYAKKNAELQGLQNNVEDYVSALSMQKNVSSNPHSGRIEEL 169

76 MEQVEALMDOKIADYAKKNAELQGLQNNVEDYVSALSMQKNVSSNPHSGRIEEL 135

DB 170 FSOAESHFNSMPSFAISGEVLFITTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFY 229

136 FSOAESHFNSMPSFAISGEVLFITTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFY 195

DB 230 KROLKLTQYTYDHCYKMYWVGDLKRGSSYESWVFNRRRMTLTVDLTLFPLYDVR 289

196 KROLKLTQYTYDHCYKMYWVGDLKRGSSYESWVFNRRRMTLTVDLTLFPLYDVR 255

DB 290 LVPKEVTELTBDVLTDPVGVNMLRGYGTFSNIENYIRKPHLPDYLRHQFHTRFQPG 349

DB 256 LVPKEVTELTBDVLTDPVGVNMLRGYGTFSNIENYIRKPHLPDYLRHQFHTRFQPG 315

|||||

RESULT 15

AA015783 standard; Protein: 1100 AA.

AA015783:

10-FEB-1992 (first entry)

B. thuringiensis toxin/AcNPV gp64 fusion protein.

chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae; midgut targeting; bacterial endotoxin; pFAV10.

Bacillus thuringiensis var. tenebriosis.

Autographa californica Nuclear Polyhedrosis Virus.

MO9117254-A.

14-NOV-1991.

02-MAY-1991: 91WO-US03008.

03-MAY-1990: 90US-0518575.

(REGC) UNIV OF CALIFORNIA.

Sivasubramanian N, Federici A;

WPI: 1991-353775/48.

N-PSDB: AA014806.

Extending host range or toxicity of insecticidal proteins - using protein capable of binding to gut epithelium of insects

Claim 55; Fig 16; 61pp; English.

A polylinker was inserted into the XmnI restriction site at the carboxyl terminus coding region of B. thuringiensis var. tenebriosis (Bt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV was operably linked to the Bt toxin coding sequence via the polylinker. The gp64 gene sequences act as midgut targeting signals for bacterial endotoxins. Of three different Bt/gp64 gene fusions that were constructed, pFAV10 was the longest. Its deduced amino acid sequence is given here.

See also AA014807 and AA014808.

Sequence 1100 AA:

Query Match 91.6%; Score 590; DB 12; Length 1100;

DB 350 YTGNDSPFNWNGVYSTRPSIGSNDITTSFYGKSKSEPVQNLFEENGKRYRAVANTNLA 409

316 YTGNDSPFNWNGVYSTRPSIGSNDITTSFYGKSKSEPVQNLFEENGKRYRAVANTNLA 375

DB 410 VMPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKGAWSMDISDLPETTDEPLEKGY 469

376 VMPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKGAWSMDISDLPETTDEPLEKGY 435

DB 470 SHQNLVWCFELMOSRGITPVLTWTHKSVDFNMIDSKITQPLVKAAYKLGASGVAVG 529

436 SHQNLVWCFELMOSRGITPVLTWTHKSVDFNMIDSKITQPLVKAAYKLGASGVAVG 495

DB 530 PRFTGGIIIOCTENGSAATITVTPDVYSQKRYARIRHASTSITTTLSLDGAPFNQYF 589

496 PRFTGGIIIOCTENGSAATITVTPDVYSQKRYARIRHASTSITTTLSLDGAPFNQYF 555

DB 590 DKTINKGDTLYNSFNFLASFSTPELSCNNLQIGVTGLSAGDKYIDKIE 639

556 DKTINKGDTLYNSFNFLASFSTPELSCNNLQIGVTGLSAGDKYIDKIE 605

Best Local Similarity 100.0%; Pred. No. 0;
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSSTTKDYIQGIVSGVGLLGVGFPFGALVSYTYNFLTNPSEDPMKAF 109
 DB 16 ADNNTALDSSSTTKDYIQGIVSGVGLLGVGFPFGALVSYTYNFLTNPSEDPMKAF 75
 QY 110 MEQVEALMDOKIADYAKKNAELQGLONNVEDYVSAISSMOKNPVSSNPHSOGIRPL 169
 DB 76 MEQVEALMDOKIADYAKKNAELQGLONNVEDYVSAISSMOKNPVSSNPHSOGIRPL 135
 QY 170 FSGAESHFNRSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGKEKEDIAEY 229
 DB 136 FSGAESHFNRSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGKEKEDIAEY 195
 QY 230 KROLKLTQETDHCWKYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVR 289
 DB 196 KROLKLTQETDHCWKYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVR 255
 QY 290 LYPKEVKTETLRDYLTPIVGVNNGRGYGTFSNTENYIRKPHLDYLRHQFHTRPOFG 349
 DB 256 LYPKEVKTETLRDYLTPIVGVNNGRGYGTFSNTENYIRKPHLDYLRHQFHTRPOFG 315
 QY 350 YYGNDSPFNWGSNGVYSTRPSIGSNDITSPFYGNKSSEPVQNLDFENGKGVYRAVANTNLA 409
 DB 316 YYGNDSPFNWGSNGVYSTRPSIGSNDITSPFYGNKSSEPVQNLDFENGKGVYRAVANTNLA 375
 QY 410 WPSAYSVGVYKVEFSQYNDQDEASTQYTDKRNKAVGWSIDOLPETTDEPLEKGY 469
 DB 376 WPSAYSVGVYKVEFSQYNDQDEASTQYTDKRNKAVGWSIDOLPETTDEPLEKGY 435
 QY 470 SHQNLVWGMFLMGSGRGTIPVLWTHKSVDFNMIDSKITLOPLVKAOKLOGSAYVAG 529
 DB 436 SHQNLVWGMFLMGSGRGTIPVLWTHKSVDFNMIDSKITLOPLVKAOKLOGSAYVAG 495
 QY 530 PRFTGGDIIOCTBENGSAATITVTPDVYSQKYRARIHVASTSQITFTSLDGAPEYQYFF 589
 DB 496 PRFTGGDIIOCTBENGSAATITVTPDVYSQKYRARIHVASTSQITFTSLDGAPEYQYFF 555
 QY 590 DRTINKGDTLTYSNFFLASFTSPFELSGNNLQIGVTLGASAGKYVIDKIE 639
 DB 556 DRTINKGDTLTYSNFFLASFTSPFELSGNNLQIGVTLGASAGKYVIDKIE 605

RESULT 16
 AAR99960
 ID AAR99960 standard: Protein: 644 AA.
 XX AAR99960:
 AC AAR99960:
 DT 04-DEC-1996 (first entry)
 XX
 DE B.t.t. coleopteran toxin (alternative N- and C-terminal truncations).
 XX
 KW Bacillus thuringiensis var. tenebrionis; insect resistance;
 KM transgenic plant; crop protection; crystal protein; toxin;
 KM Coleoptera.
 XX
 OS Bacillus thuringiensis var. tenebrionis.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 48 /note= "N-terminus of construct 5456"
 FT MISC-difference 77 /note= "N-terminus of construct 5452"
 FT MISC-difference 99 /note= "N-terminus of construct 5467"
 FT MISC-difference 490 /note= "C-terminus of construct 5438"
 FT MISC-difference 536 /note= "C-terminus of construct 5441"
 FT MISC-difference 582 /note= "C-terminus of construct 5449"

FT MISC-difference 640 /note= "C-terminus of construct 5448"
 FT
 XX
 PN EP731170-A1.
 XX
 PD 11-SEP-1996.
 XX
 PE 26-APR-1988; 88EP-0870070.
 XX
 PR 29-APR-1987; 87US-0044081.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Fischhoff DA, Fuchs RL, Lavrik PB, McPherson SA;
 PI Petlak FU;
 DR WPI: 1996-403991/41.
 XX
 PT Chimeric plant gene which expresses a Bacillus thuringiensis toxin
 PT protein - useful for prodn. of plants which are toxic to
 PT Coleopteran Insects
 PS
 XX
 SS Disclosure: Fig 10; 72pp; English.
 CC
 CC The effects of N- and C-terminal deletions (AAR99960) on the toxicity
 CC of the Coleopteran toxin (see also AAR99958) of Bacillus thuringiensis
 CC var. tenebrionis (B.t.t.) were examined. Mutant genes were expressed
 CC in E. coli and the truncated proteins were tested for activity against
 CC Colorado potato beetle. All the C-terminal truncations, even of
 CC only 4 amino acids (construct 5448), resulted in a loss of activity.
 CC The N-terminus of the toxin was more tolerant; a mutant toxin
 CC deleted of 76 amino acids (construct 5452) exhibited toxicity.
 CC However, a deletion of 99 amino acids (construct 5467) resulted in
 CC loss of activity.
 CC
 XX
 SQ Sequence 644 AA;
 Query Match 84.3%; Score 543; DB 17; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPPTLEDLYKEFLMTADNNTALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPPTLEDLYKEFLMTADNNTALDSS 60
 QY 61 TTKVYIQGIVSGVGLLGVGFPFGALVSYTYNFLTNPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKVYIQGIVSGVGLLGVGFPFGALVSYTYNFLTNPSEDPMKAFMEQVEALMDOK 120
 QY 121 IADYAKKNAELQGLONNVEDYVSAISSMOKNPVSSNPHSOGRIREFSQAESHFRNS 180
 DB 121 IADYAKKNAELQGLONNVEDYVSAISSMOKNPVSSNPHSOGRIREFSQAESHFRNS 180
 QY 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGKEKEDIAEYKROLKLTQEXT 240
 DB 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGKEKEDIAEYKROLKLTQEXT 240
 QY 241 DHCWKYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVRLYPREVTELT 300
 DB 241 DHCWKYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVRLYPREVTELT 300
 QY 301 RDVLTDPYIVGVNNGRGYGTFSNTENYIRKPHLDYLRHQFHTRPOGYGNDSPFNYS 360
 DB 301 RDVLTDPYIVGVNNGRGYGTFSNTENYIRKPHLDYLRHQFHTRPOGYGNDSPFNYS 360
 QY 361 GNVYSTRPSIGSNDITSPFYGNKSSEPVQNLDFENGKGVYRAVANTNLAVPSAVYSGVT 420
 DB 361 GNVYSTRPSIGSNDITSPFYGNKSSEPVQNLDFENGKGVYRAVANTNLAVPSAVYSGVT 420
 QY 421 KVEFSQYNDQDEASTQYTDKRNKAVGWSIDOLPETTDEPLEKGYSHQNLVWGMFL 480
 DB 421 KVEFSQYNDQDEASTQYTDKRNKAVGWSIDOLPETTDEPLEKGYSHQNLVWGMFL 480


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FH Key Location/Qualifiers
FT Misc-difference 251 /label= L251A
FT /note= "wild type Leu replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34813-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards
XX Diabrotica virgifera. The toxicity of the present sequence towards
XX Diabrotica virgifera was tested. The EC50 value (concentration at which
XX 50% feeding inhibition is observed) of the present protein was found to
XX be 5.27 microgram per millilitre, compared to 7.45 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA:
SQ
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNNRSHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
DB 1 MNPNNRSHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
QY 61 TTKDVIQGISVVDLLGVGFPFGALVSYFTNLTIMPSDEPKAFMEQVVALMDOK 120
DB 61 TTKDVIQGISVVDLLGVGFPFGALVSYFTNLTIMPSDEPKAFMEQVVALMDOK 120
QY 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPSSRNPHSOGRIRELSQAESHPRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPSSRNPHSOGRIRELSQAESHPRNS 180
QY 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPSSRNPHSOGRIRELSQAESHPRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPSSRNPHSOGRIRELSQAESHPRNS 180
QY 181 MPSPAIISGYEVLFTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEYT 240
DB 181 MPSPAIISGYEVLFTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEYT 240
QY 181 MPSPAIISGYEVLFTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEYT 240
DB 181 MPSPAIISGYEVLFTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEYT 240
QY 241 DHCKWNTNVGLDKRGSSYSWVNFNRYRREMTLVLDLALPLVYRIRPREVKTELT 300
DB 241 DHCKWNTNVGLDKRGSSYSWVNFNRYRREMTLVLDLALPLVYRIRPREVKTELT 300
QY 301 RDVLTDPYGVNMLRGYGTFTSNIENYIRKPHLFYDLHRIQFTRPQGYGNDSEFNYS 360
DB 301 RDVLTDPYGVNMLRGYGTFTSNIENYIRKPHLFYDLHRIQFTRPQGYGNDSEFNYS 360

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QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEPNGEKYTRAVANTMLAWPSAVISGVT 420
DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEPNGEKYTRAVANTMLAWPSAVISGVT 420
QY 421 KVEFSQYNDQDEASTQYDYSKRNAGVAVSMDSIDQLPETTDEPLEKGYSHOLNVMWCF 480
DB 421 KVEFSQYNDQDEASTQYDYSKRNAGVAVSMDSIDQLPETTDEPLEKGYSHOLNVMWCF 480
QY 481 MGSRGITPVLTWTHKSVDEFNMIDSKKITQLPLVKAAYKLQSGASVAVGPRFTGDIIOC 540
DB 481 MGSRGITPVLTWTHKSVDEFNMIDSKKITQLPLVKAAYKLQSGASVAVGPRFTGDIIOC 540
QY 541 TENGSAAITVTPDVVSQKXRRARIRHASTQITFTLSLDCGAPNNOYFPKTKINKGDTLT 600
DB 541 TENGSAAITVTPDVVSQKXRRARIRHASTQITFTLSLDCGAPNNOYFPKTKINKGDTLT 600
QY 601 YNSFNLSFSTPELSCNNLQIGVTGSLADKVIYDIKIEFIPVN 644
DB 601 YNSFNLSFSTPELSCNNLQIGVTGSLADKVIYDIKIEFIPVN 644

RESULT 19
AAW34813
ID AAW34813 standard; Protein; 644 AA.
AC AAW34813;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein G352A.
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
OS
FH Key Location/Qualifiers
FT Misc-difference 352 /label= G352A
FT /note= "wild type Gly replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34813-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

```

CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards *Diabrotica*
 CC *virgifera* was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 4.11 microgram per millilitre, compared to 7.45 microgram per
 CC millilitre for the wild type *CryIIIA* protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MNPNNSEHDTIKTTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTTEALDSS 60
   |||
DB 1 MNPNNSEHDTIKTTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTTEALDSS 60
   |||
OY 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
   |||
DB 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
   |||
OY 121 IADYAKKALAELOGLONNEDVVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
   |||
DB 121 IADYAKKALAELOGLONNEDVVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
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OY 181 MPFSAISGYEVLFLTYAQAANTHFLKDAQIYGEWGEKEDIKFKROLKLTQEXT 240
   |||
DB 181 MPFSAISGYEVLFLTYAQAANTHFLKDAQIYGEWGEKEDIKFKROLKLTQEXT 240
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OY 241 DHCWKYVNGDLKRGSSYSWVNFNRYRREMTLTVLDIALPPLVDVRLPKREVTTELT 300
   |||
DB 241 DHCWKYVNGDLKRGSSYSWVNFNRYRREMTLTVLDIALPPLVDVRLPKREVTTELT 300
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OY 301 RDVLTIDIVGVNRLRGYTFNSNTENYIRKPHLEFDYLRHQFTFRPOGYGNDSEFYMS 360
   |||
DB 301 RDVLTIDIVGVNRLRGYTFNSNTENYIRKPHLEFDYLRHQFTFRPOGYGNDSEFYMS 360
   |||
OY 361 GNYVSTRPSIGSNDITSPFYGNKSEPPVONLEFNGEKYRVAANTNLAWPSAVYSGVT 420
   |||
DB 361 GNYVSTRPSIGSNDITSPFYGNKSEPPVONLEFNGEKYRVAANTNLAWPSAVYSGVT 420
   |||
OY 421 KVESQVNDQDEASTQTYSKRVAGVSMDSIDQLPETTDEPLEGYSHQLNTYWCFL 480
   |||
DB 421 KVESQVNDQDEASTQTYSKRVAGVSMDSIDQLPETTDEPLEGYSHQLNTYWCFL 480
   |||
OY 481 MQGSRGTIPVLTHKSVDFEFNMIDSKKITQLPLVKAYKLQSGASVAVAGPRTGGDIIQC 540
   |||
DB 481 MQGSRGTIPVLTHKSVDFEFNMIDSKKITQLPLVKAYKLQSGASVAVAGPRTGGDIIQC 540
   |||
OY 541 TENGSAATIVTPPVYSQKRAIRIHAASQTFTTSLDGAEPNQQYFFPKTINKGDTLT 600
   |||
DB 541 TENGSAATIVTPPVYSQKRAIRIHAASQTFTTSLDGAEPNQQYFFPKTINKGDTLT 600
   |||
OY 601 YNSFNLASFTPELSGNNLOIGTGLSAGDKYIDIKIEFIPVN 644
   |||
DB 601 YNSFNLASFTPELSGNNLOIGTGLSAGDKYIDIKIEFIPVN 644
   |||

```

RESULT 20

AAW34814 ID AAW34814 standard; protein: 644 AA.

AAW34814:

25-FEB-1998 (first entry)

Novel *CryIIIA* mutant protein N353A.

KM *CryIIIA* gene: corn rootworm toxicity; *CryIIIA* protein:
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;

KW *Diabrotica virgifera virgifera*.

XX Synthetic.
 OS *Bacillus thuringiensis*.

XX Key location/Qualifiers

FT Misc-difference 353 /label= N353A
 FT /note= "wild type Asn replaced with Ala"

PN US5659123-A.

PD 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

PA (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Jansens S, Peferoen M, Van Rie J;

DR WPI, 1997-424316/39.

PT Modified *Bacillus thuringiensis* *CryIIIA* proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

PS Example 1; Page -: 22pp; English.

CC Novel *CryIIIA* proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the *CryIIIA* protein of *Bacillus*
 CC *thuringiensis*. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel *CryIIIA* proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards *Diabrotica*
 CC *virgifera* was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 5.21 microgram per millilitre, compared to 11.60 microgram per
 CC millilitre for the wild type *CryIIIA* protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MNPNNSEHDTIKTTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTTEALDSS 60
   |||
DB 1 MNPNNSEHDTIKTTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTTEALDSS 60
   |||
OY 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
   |||
DB 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
   |||
OY 121 IADYAKKALAELOGLONNEDVVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
   |||
DB 121 IADYAKKALAELOGLONNEDVVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
   |||
OY 181 MPFSAISGYEVLFLTYAQAANTHFLKDAQIYGEWGEKEDIKFKROLKLTQEXT 240
   |||
DB 181 MPFSAISGYEVLFLTYAQAANTHFLKDAQIYGEWGEKEDIKFKROLKLTQEXT 240
   |||
OY 241 DHCWKYVNGDLKRGSSYSWVNFNRYRREMTLTVLDIALPPLVDVRLPKREVTTELT 300
   |||
DB 241 DHCWKYVNGDLKRGSSYSWVNFNRYRREMTLTVLDIALPPLVDVRLPKREVTTELT 300
   |||

```



```

DE Novel CryIIIA mutant protein P412A.
XX
XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleoptera insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FH Misc-difference 412
FT /label= "P412A
ET /note= "wild type Pro replaced with Ala"
XX
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rle J;
XX
XX WP1; 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleoptera insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
XX Claim 9; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleoptera insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be >243 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein. This mutant protein is
CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The
CC toxicity of the mutant protein for this Diabrotica pest was
CC significantly below the toxicity of the native CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
XX
S0 Sequence 644 AA:
XX
XX Query Match 84.3%; Score 543; DB 18; Length 644;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX
XX 1 MNPNNRSEHDTIKTETNNEVPNTNHQVPLAETPNPTLEDLNTKELRMTADNNTTEALDSS 60
XX | MNPNNRSEHDTIKTETNNEVPNTNHQVPLAETPNPTLEDLNTKELRMTADNNTTEALDSS 60
XX
XX 61 TTKDVIQKISVYGDLGVGFPFGALVSFTYNTINTWPSDEPWKAFMEOVEALMDOK 120
XX | TTKDVIQKISVYGDLGVGFPFGALVSFTYNTINTWPSDEPWKAFMEOVEALMDOK 120
XX
XX 61 TTKDVIQKISVYGDLGVGFPFGALVSFTYNTINTWPSDEPWKAFMEOVEALMDOK 120
XX | TTKDVIQKISVYGDLGVGFPFGALVSFTYNTINTWPSDEPWKAFMEOVEALMDOK 120
XX
XX 121 INDVKNKKALAEQGLQNNVEDIVSALSSQKNPNVSRNPHSOGRTRELFSQESHFRNS 180
XX | INDVKNKKALAEQGLQNNVEDIVSALSSQKNPNVSRNPHSOGRTRELFSQESHFRNS 180
XX
XX 121 INDVKNKKALAEQGLQNNVEDIVSALSSQKNPNVSRNPHSOGRTRELFSQESHFRNS 180
XX | INDVKNKKALAEQGLQNNVEDIVSALSSQKNPNVSRNPHSOGRTRELFSQESHFRNS 180

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PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards *Diabrotica*
CC *virgifera virgifera* was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.93 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

SO Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDITKTENNENVPNTNHVQYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNTNHVQYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
OY 61 TTKDVIOKGISVVDLLGVGFPFGALVSFTNFTLNTMPSEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIOKGISVVDLLGVGFPFGALVSFTNFTLNTMPSEDPKAFMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFSAESHFRNS 180
DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFSAESHFRNS 180
OY 181 MPSEFASGYEVLFETTYAQAAMTHFLKDAQIYGEWGEKEDIAEFKROKLKTQEXT 240
DB 181 MPSEFASGYEVLFETTYAQAAMTHFLKDAQIYGEWGEKEDIAEFKROKLKTQEXT 240
OY 241 DHCVKMYNYGLDKLRGSSYESWVNFNRREMTLVLDLIAFPPLYDVALYKEVTELT 300
DB 241 DHCVKMYNYGLDKLRGSSYESWVNFNRREMTLVLDLIAFPPLYDVALYKEVTELT 300
OY 301 RDVLTPIYGVNNLRGTYGTFPSNIENYIRKPHLEFYLRIQFTRPPQGYGNDSPFNWS 360
DB 301 RDVLTPIYGVNNLRGTYGTFPSNIENYIRKPHLEFYLRIQFTRPPQGYGNDSPFNWS 360
OY 361 GNVSTRPSIGSNDITTSFYGKSEPVQNLFEENGEXYRAVANINLAWVSAVYSGVT 420
DB 361 GNVSTRPSIGSNDITTSFYGKSEPVQNLFEENGEXYRAVANINLAWVSAVYSGVT 420
OY 421 KVEFSQYNDQDEASTQYDSCRNGAVSWDSIDQLPETTDEPLEKGYSHQLNVVMCL 480
DB 421 KVEFSQYNDQDEASTQYDSCRNGAVSWDSIDQLPETTDEPLEKGYSHQLNVVMCL 480
OY 481 MGSGRITIVLVTHKSVFFNMIDSKITPOLPLVAKYKLGASGAVAGPRTGGDIIQC 540
DB 481 MGSGRITIVLVTHKSVFFNMIDSKITPOLPLVAKYKLGASGAVAGPRTGGDIIQC 540
OY 541 TENGSAATITVTPDVYSKYRARIHYASTSQTITFLSLDGAPEMQYFDKTIKNGDILT 600
DB 541 TENGSAATITVTPDVYSKYRARIHYASTSQTITFLSLDGAPEMQYFDKTIKNGDILT 600
OY 601 YNSFNLSFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLSFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 24

AAW34818
ID AAW34818 standard; Protein: 644 AA.

XX AAW34818;

XX 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein Q482A.

XX CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
XX *Diabrotica virgifera virgifera*.

OS Synthetic.
XX *Bacillus thuringiensis*.

XX Key Location/Qualifiers
FT Misc-difference 482
FT /label="Q482A
FT /note="wild type Gln replaced with Ala"

XX US659123-A.

XX 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

XX (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Jansens S, Peferoen M, Van Rie J;

XX WPI: 1997-424316/39.

PT Modified *Bacillus thuringiensis* CryIIIA proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle

PS Example 1; Page -: 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards *Diabrotica*
CC *virgifera virgifera* was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.96 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

XX Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDITKTENNENVPNTNHVQYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNTNHVQYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
OY 61 TTKDVIOKGISVVDLLGVGFPFGALVSFTNFTLNTMPSEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIOKGISVVDLLGVGFPFGALVSFTNFTLNTMPSEDPKAFMEQVEALMDOK 120


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|||||
Db 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
QY 601 YNSFNLASFTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASFTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 26
AAW34820
ID AAW34820 standard: Protein: 644 AA.
XX
AC AAW34820:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein T406A.
XX
KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KM increased toxicity; Coleopteran insect; Colorado potato beetle;
KM relative solvent accessibility; plant resistance;
KM Diabrotica virgifera virgifera.
XX
OS Synthetic.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 406 /label= T406A
FT /note= "wild type Thr replaced with Ala"
FT
FT
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW3481-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards insects.
XX Specifically, the toxicity of the present sequence towards Diabrotica
XX virgifera virgifera was tested. The EC50 value (concentration at which
XX 50% feeding inhibition is observed) of the present protein was found to
XX be 5.50 microgram per millilitre, compared to 2.42 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA:
XX
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;

```

```

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDTIKTTENNENVTNNHQQYPLAETPPTLEDLNYKEEFLMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNENVTNNHQQYPLAETPPTLEDLNYKEEFLMTADNNTALDSS 60
QY 61 TTKVDYIOKGISVYVDLLGVGFFPGGALVSEFYTNFLNTIPSPEDPKAFMEQVEALMDCK 120
Db 61 TTKVDYIOKGISVYVDLLGVGFFPGGALVSEFYTNFLNTIPSPEDPKAFMEQVEALMDCK 120
QY 121 IADYAKKKALAELOGLONNEDYVSALSSWQKPNVSSRNPHSGGRITRELSQAESHPRNS 180
Db 121 IADYAKKKALAELOGLONNEDYVSALSSWQKPNVSSRNPHSGGRITRELSQAESHPRNS 180
QY 181 MPEFAISGEYVLEFTTYAQAANTHLEFLKDAQIYGEEMGYEKEDIAEFYKROQLTQEXT 240
Db 181 MPEFAISGEYVLEFTTYAQAANTHLEFLKDAQIYGEEMGYEKEDIAEFYKROQLTQEXT 240
QY 241 DHCKWYNVGLDKRGSSYSWVNFNRYREEMTLTVLDLALFPLVDVRLYREXVTELT 300
Db 241 DHCKWYNVGLDKRGSSYSWVNFNRYREEMTLTVLDLALFPLVDVRLYREXVTELT 300
QY 301 RDVLTDPVGVNMLRGYGTFFSNIENTYIRKPHLEFDYLRIOFTRPOPGYGGDSFNYS 360
Db 301 RDVLTDPVGVNMLRGYGTFFSNIENTYIRKPHLEFDYLRIOFTRPOPGYGGDSFNYS 360
QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSDPVONLEFNGEKYYRAVANNTLAWPSAVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSSDPVONLEFNGEKYYRAVANNTLAWPSAVYSGVT 420
QY 421 KVEFSQYNDQTDASTQTTDSKRNQGVSWDSIDQLPPEPTDPLEKGYSHQUNYMCFL 480
Db 421 KVEFSQYNDQTDASTQTTDSKRNQGVSWDSIDQLPPEPTDPLEKGYSHQUNYMCFL 480
QY 481 MGSRGITIPVLTWTHKSVDFEFNMIDSKITQLPLVAVAYKLQSGASVVAAPRFTGGDIIOC 540
Db 481 MGSRGITIPVLTWTHKSVDFEFNMIDSKITQLPLVAVAYKLQSGASVVAAPRFTGGDIIOC 540
QY 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
Db 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
QY 601 YNSFNLASFTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASFTPELISGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 27
AAW34821
ID AAW34821 standard: Protein: 644 AA.
XX
AC AAW34821:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein G349A.
XX
XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX increased toxicity; Coleopteran insect; Colorado potato beetle;
XX relative solvent accessibility; plant resistance;
XX Diabrotica virgifera virgifera.
XX
XX Synthetic.
XX
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 349 /label= G349A
FT /note= "wild type Gly replaced with Ala"
FT
FT
XX
XX US5659123-A.
XX
XX 19-AUG-1997.

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Pf	26-AUG-1994;	94US-0295060.
XX		
XX	26-AUG-1994;	94US-0295060.
PR		
PA	(PLBZ) PLANT GENETIC SYSTEMS NV.	
XX		
PI	Jansens S, Peferoen M, Van Rle J;	
DR	WPI; 1997-424316/39.	
XX		
PT	Modified Bacillus thuringiensis CryIII proteins - with increased	
PT	toxicity against insect pests, particularly Coleopteran insects,	
XX	e.g. corn rootworm and Colorado potato beetle	
PS	Claim 9; Page -: 22pp; English.	
XX		
CC	Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning	
CC	mutagenesis of domain II of the CryIIIA protein of Bacillus	
CC	thuringiensis. All the positions changed to alanine in these proteins	
CC	are located in some of the solvent exposed loops and beta-strands	
CC	directed towards or located at the molecular apex. The substituted amino	
CC	acids have a relative solvent accessibility of at least 40%, or are a	
CC	maximum distance of 3 amino acids away from an amino acid having at least	
CC	40% relative solvent accessibility. The novel CryIIIA proteins have an	
CC	increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,	
CC	and can be used to combat, or improve plant resistance towards insects.	
CC	Specifically, the toxicity of the present sequence towards Diabrotica	
CC	virgifera virgifera was tested. The EC50 value (concentration at which	
CC	50% feeding inhibition is observed) of the present protein was found to	
CC	be >243 microgram per millilitre, compared to 2.42 microgram per	
CC	millilitre for the wild type CryIIIA protein. This mutant protein is	
CC	recognised as a "down mutant" for Diabrotica virgifera virgifera. The	
CC	toxicity of the mutant protein for this Diabrotica pest was	
CC	significantly below the toxicity of the native CryIIIA protein.	
CC	Note: this sequence does not appear in the specification; it was created	
CC	using information provided.	
XX		
SQ	Sequence 644 AA:	
	Query Match 84.3%; Score 543; DB 18; Length 644;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0.	
OY	1 NNPNNRSEHDITIKTTENNEVPNTNHVOYLAEETPNPLEDLANKKEFLRMADNNTLEADSS 60	
DB	1 NMPNRSEHDTIKTTENNEVPNTNHVOYLAEETPNPLEDLANKKEFLRMADNNTLEADSS 60	
OY	61 TTKDVIQKGISVYGDLGVGFPFGGALVSFTTNFNTIWPSEDDEPKAKMEOVEALMDOK 120	
DB	61 TTKDVIQKGISVYGDLGVGFPFGGALVSFTTNFNTIWPSEDDEPKAKMEOVEALMDOK 120	
OY	121 IADYKKNKRLAELQGLONNVEDYVSALSSWMKNPVSSRRPHSGGRIRLEFSQAESHFRNS 180	
DB	121 IADYKKNKRLAELQGLONNVEDYVSALSSWMKNPVSSRRPHSGGRIRLEFSQAESHFRNS 180	
OY	181 MPSPAISGEVEFLTTYAQANATHFLDLDAQIYGEEMGYEKEDIAEFKRKQLKLQEYT 240	
DB	181 MPSPAISGEVEFLTTYAQANATHFLDLDAQIYGEEMGYEKEDIAEFKRKQLKLQEYT 240	
OY	241 DHCVMYANGDLKLGSSSYESVWNFRRYREMTLVLDLIALPPLYDVRLYPREVKTELT 300	
DB	241 DHCVMYANGDLKLGSSSYESVWNFRRYREMTLVLDLIALPPLYDVRLYPREVKTELT 300	
OY	301 ROVLNDPIYGVNNLKGYSGTTFSTNIENYIRKPHLFVLRHQFTTRPOGYGDSFNWMS 360	
DB	301 ROVLNDPIYGVNNLKGYSGTTFSTNIENYIRKPHLFVLRHQFTTRPOGYGDSFNWMS 360	
OY	361 GNVTSTRPSIGSNDDITTSFYGNKSSEPQNOLFENEKERYRAVANLNLLVWPSAVSYGYT 420	
DB	361 GNVTSTRPSIGSNDDITTSFYGNKSSEPQNOLFENEKERYRAVANLNLLVWPSAVSYGYT 420	
OY	421 KVFESQYNDQJDEASTQTQYDSCRNKGAVSWSDSIDQLPETTBDEPLEKGYSHOLINVMCL 480	

Db 421 KVERSOYNQDTDEASIQGTYSKRNKVCASWMSIDQLPETTDEPLEKGYSHQLNVMCFL 480
|||||
Qy 481 MQGSRGTIPVLWTHKSVDFEFNKIDSKITTLQPLVKATKLGSGASVAVAGPFTGGDIIOC 540
Db 481 MQGSRGTIPVLWTHKSVDFEFNKIDSKITTLQPLVKATKLGSGASVAVAGPFTGGDIIOC 540
Qy 541 TENNSAATITVTPDVSQKRYRARIHYASTSQTITFLSLDGAPEFQOYFEDTKINKGDTLT 600
Db 541 TENNSAATITVTPDVSQKRYRARIHYASTSQTITFLSLDGAPEFQOYFEDTKINKGDTLT 600
Qy 601 YNSFNLASFSTPELGSNNLQIGVTLASGDVYVYIDKIEFIPVN 644
Db 601 YNSFNLASFSTPELGSNNLQIGVTLASGDVYVYIDKIEFIPVN 644

RESULT 28
AAM34822
ID AAM34822 standard; Protein; 644 AA.
XX
AC AAM34822;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein V311A.
XX
KW cryIIIA gene: corn rootworm toxicity; CryIIIA protein;
RW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FH MISC-difference 311
FT /label= V311A
FT /note= "wild type Val replaced with Ala"
XX
XX US5659123-A.
PN
PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLBZ) PLANT GENETIC SYSTEMS NV.
PI Jansens S, Peferoen M, Van Rie J;
PI
DR WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.09 microgram per millilitre, compared to 1.21 microgram per

CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDITKTENNENVTNHOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
DB 1 MNPNNRSEHDITKTENNENVTNHOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
QY 61 TTKDVIOKGISVVGDLGVGFPFGGALVSFTYNFLNTIPSEDPWKAEMEVEALMDOK 120
DB 61 TTKDVIOKGISVVGDLGVGFPFGGALVSFTYNFLNTIPSEDPWKAEMEVEALMDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
QY 181 MPSFAISGEVLEFLTTTAAQANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
DB 181 MPSFAISGEVLEFLTTTAAQANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
QY 241 DHCVKMYNVLGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDRLYKPKYKTELT 300
DB 241 DHCVKMYNVLGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDRLYKPKYKTELT 300
QY 301 RDVLTDPVIGVNNLRGCGTTFSSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYMS 360
DB 301 RDVLTDPVIGVNNLRGCGTTFSSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYMS 360
QY 361 GNVYSRPSIGSNDITTSFYGNKSEPEYQNLFEFGKRYAVANTNLAWPSAVSYGYT 420
DB 361 GNVYSRPSIGSNDITTSFYGNKSEPEYQNLFEFGKRYAVANTNLAWPSAVSYGYT 420
QY 421 KYEFSQYNDQDEASTQYTDKSRNGAVSMDSIDQLPETDEPLEKGYSHOANVMCFU 480
DB 421 KYEFSQYNDQDEASTQYTDKSRNGAVSMDSIDQLPETDEPLEKGYSHOANVMCFU 480
QY 481 MGSGRGTIVLTWTHKSVDFEWMIDSKITQLPLVKAAYKLOGSASVAGPRETGGDITQC 540
DB 481 MGSGRGTIVLTWTHKSVDFEWMIDSKITQLPLVKAAYKLOGSASVAGPRETGGDITQC 540
QY 541 TENGSAATYVTPDVSYSQYRARIHYASTSQITFTLSIDGAPFNOYQYEDKTINKGDILT 600
DB 541 TENGSAATYVTPDVSYSQYRARIHYASTSQITFTLSIDGAPFNOYQYEDKTINKGDILT 600
QY 601 YNSFNLASFPPELSCGNLQIGVGLSAGDKVYIDKIEFIIPVN 644
DB 601 YNSFNLASFPPELSCGNLQIGVGLSAGDKVYIDKIEFIIPVN 644

```

RESULT 29
 AAM34823
 ID AAM34823 standard; Protein: 644 AA.

XX AAM34823;

XX 25-FEB-1998 (first entry)

XX Novel CryIIIA mutant protein N312A.

XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 XX increased toxicity; Coleopteran insect; Colorado potato beetle;
 XX relative solvent accessibility; plant resistance;
 XX Diabrotica virgifera virgifera.

OS Synthetic.
 OS Bacillus thuringiensis.
 XX

FFH Key Location/Qualifiers
 FFH Misc-difference 312 /label= N312A
 FFH /note= "wild type Asn replaced with Ala"

XX US5659123-A.

XX 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

XX (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Janssens S, Peferoen M, Van Rie J;

XX WPI: 1997-424316/39.

PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

XX Example 1; Page -: 22pp; English.

CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.65 microgram per millilitre, compared to 1.21 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDITKTENNENVTNHOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
DB 1 MNPNNRSEHDITKTENNENVTNHOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
QY 61 TTKDVIOKGISVVGDLGVGFPFGGALVSFTYNFLNTIPSEDPWKAEMEVEALMDOK 120
DB 61 TTKDVIOKGISVVGDLGVGFPFGGALVSFTYNFLNTIPSEDPWKAEMEVEALMDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
QY 181 MPSFAISGEVLEFLTTTAAQANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
DB 181 MPSFAISGEVLEFLTTTAAQANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
QY 241 DHCVKMYNVLGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDRLYKPKYKTELT 300
DB 241 DHCVKMYNVLGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDRLYKPKYKTELT 300
QY 301 RDVLTDPVIGVNNLRGCGTTFSSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYMS 360
DB 301 RDVLTDPVIGVNNLRGCGTTFSSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYMS 360

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QY 361 GNYSTRPSISNDITTSPEYGNKSSPEPVONLENGEKYRAVANTNLAVPSAVYSGVT 420
 CC 361 GNYSTRPSISNDITTSPEYGNKSSPEPVONLENGEKYRAVANTNLAVPSAVYSGVT 420
 Db 361 GNYSTRPSISNDITTSPEYGNKSSPEPVONLENGEKYRAVANTNLAVPSAVYSGVT 420
 QY 421 KYEFSQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 CC 421 KYEFSQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 Db 421 KYEFSQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 QY 481 MGSRGITPVLWTWTKHSVDFEPMIDSKKITOLPLVKAKYKLGSGASVYAGPRTGGDIQC 540
 CC 481 MGSRGITPVLWTWTKHSVDFEPMIDSKKITOLPLVKAKYKLGSGASVYAGPRTGGDIQC 540
 Db 481 MGSRGITPVLWTWTKHSVDFEPMIDSKKITOLPLVKAKYKLGSGASVYAGPRTGGDIQC 540
 QY 541 TENGSAATITVTPDVYSQYKRRARIHVASTQITFTLSLDGAPFQYFEDTINKGDTLT 600
 CC 541 TENGSAATITVTPDVYSQYKRRARIHVASTQITFTLSLDGAPFQYFEDTINKGDTLT 600
 Db 541 TENGSAATITVTPDVYSQYKRRARIHVASTQITFTLSLDGAPFQYFEDTINKGDTLT 600
 QY 601 YNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 CC 601 YNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 601 YNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 30
 AAM34824
 ID AAM34824 standard; Protein: 644 AA.
 XX
 AC AAM34824;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein N326A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 326
 FT /label= N326A
 FT /note="Wild type Asn replaced with Ala"
 FT
 XX
 PN US5659123-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI; 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1: Page -: 22pp; English.
 XX
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 7.80 microgram per millilitre, compared to 2.40 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX
 SQ Sequence 644 AA:
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPNTNHVQPLAETPPTLEDLNTYKEFLBMTADNNTALDSS 60
 Db 1 MNPNNRSEHDTIKTTENNEVPNTNHVQPLAETPPTLEDLNTYKEFLBMTADNNTALDSS 60
 QY 61 TTKDVIOKGISVGDLLGVVGFPPGALVSFTYNTLTIWPSDEDPKAFMEQVEALMDOK 120
 Db 61 TTKDVIOKGISVGDLLGVVGFPPGALVSFTYNTLTIWPSDEDPKAFMEQVEALMDOK 120
 QY 121 IADYAKKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSOGRIREFLSQAESHRNS 180
 Db 121 IADYAKKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSOGRIREFLSQAESHRNS 180
 QY 181 MPSPRISGEVLEFLTTTAAQAAANTHLFLKDAQITGEMGEYKEDIAEFYRQOLKQOET 240
 Db 181 MPSPRISGEVLEFLTTTAAQAAANTHLFLKDAQITGEMGEYKEDIAEFYRQOLKQOET 240
 QY 241 DHCKWYVWGLDKRGSSYESWVNFNRRREMTLTVDLALPFLYDVRLYPKVEKTEL 300
 Db 241 DHCKWYVWGLDKRGSSYESWVNFNRRREMTLTVDLALPFLYDVRLYPKVEKTEL 300
 QY 301 RDVLTDPITVGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHRFQPGYGNDSFNWYS 360
 Db 301 RDVLTDPITVGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHRFQPGYGNDSFNWYS 360
 QY 361 GNYSTRPSISNDITTSPEYGNKSSPEPVONLENGEKYRAVANTNLAVPSAVYSGVT 420
 Db 361 GNYSTRPSISNDITTSPEYGNKSSPEPVONLENGEKYRAVANTNLAVPSAVYSGVT 420
 QY 421 KYEFSQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 Db 421 KYEFSQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 QY 481 MGSRGITPVLWTWTKHSVDFEPMIDSKKITOLPLVKAKYKLGSGASVYAGPRTGGDIQC 540
 Db 481 MGSRGITPVLWTWTKHSVDFEPMIDSKKITOLPLVKAKYKLGSGASVYAGPRTGGDIQC 540
 QY 541 TENGSAATITVTPDVYSQYKRRARIHVASTQITFTLSLDGAPFQYFEDTINKGDTLT 600
 Db 541 TENGSAATITVTPDVYSQYKRRARIHVASTQITFTLSLDGAPFQYFEDTINKGDTLT 600
 QY 601 YNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 601 YNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 31
 AAM34825
 ID AAM34825 standard; Protein: 644 AA.
 XX
 AC AAM34825;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein E387A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;

Qy	301	RDVLTDDITGVNNLRGVTGTFESNIENYIKRPHLFDYLRHQHTHFQPCGYTGNDSEFWTS	366
Db	301	RDVLTDDITGVNNLRGVTGTFESNIENYIKRPHLFDYLRHQHTHFQPCGYTGNDSEFWTS	366
Qy	361	GNVYSTRPDSIGSNDITTSPEYGNKSSSEPVQNLFEFGKEKYRAVANTNLAVMPSAVSGVT	4220
Db	361	GNVYSTRPDSIGSNDITTSPEYGNKSSAPQNLFEFGKEKYRAVANTNLAVMPSAVSGVT	4220
Qy	421	KVESSQVNDQTDASVQTQVDSKRNGAVAWSIDQLPETTDEPLEKCYSHQLNVMCFL	4800
Db	421	KVESSQVNDQTDASVQTQVDSKRNGAVAWSIDQLPETTDEPLEKCYSHQLNVMCFL	4800
Qy	481	MQSGRGITPVLTTTHKSVDFEFNMIDSKKITQLPLVKAKKLQSGASVAVGPRFTGCDITQC	5400
Db	481	MQSGRGITPVLTTTHKSVDFEFNMIDSKKITQLPLVKAKKLQSGASVAVGPRFTGCDITQC	5400
Qy	541	TENGSAATITVTPDVSYTSOKRYARLRHVASTQITFTTSLDGAPEQNOYFEDKTIKGGDTLT	6000
Db	541	TENGSAATITVTPDVSYTSOKRYARLRHVASTQITFTTSLDGAPEQNOYFEDKTIKGGDTLT	6000
Qy	601	YNSFNLASFTSPPELSGNNLQIGVTGSLSGADKVYTDKIEFIIPVN 644	
Db	601	YNSFNLASFTSPPELSGNNLQIGVTGSLSGADKVYTDKIEFIIPVN 644	
RESULT 32			
AAW34826			
XX	AAW34826	standard; Protein: 644 AA.	
XX	AAW34826;		
DT	25-FEB-1998	(first entry)	
DE	Novel CryIIIA mutant protein K384A.		
XX			
KM	CryIIIA gene: corn rootworm toxicity; CryIIIA protein;		
KM	increased toxicity; Coleopteran insect; Colorado potato beetle;		
KM	relative solvent accessibility; plant resistance;		
XX	Diabrotica virgifera virgifera.		
OS	Synthetic.		
OS	Bacillus thuringiensis.		
FH	Key	Location/Qualifiers	
FT	Misc-difference 384	//label= K384A	
FT		//note= "wild type lys replaced with Ala"	
XX			
PN	US5659123-A.		
XX			
PD	19-AUG-1997.		
XX			
PE	26-AUG-1994; 94US-0295060.		
XX			
XX	26-AUG-1994; 94US-0295060.		
PA	(PLBZ) PLANT GENETIC SYSTEMS NY.		
XX			
XX	Janssens S, Peferoen M, Van Rie J;		
DR	WPT. 1997-424316/39.		
PT	Modified Bacillus thuringiensis CryIII proteins - with increased		
PT	toxicity against insect pests, particularly Coleopteran insects,		
PT	e.g. corn rootworm and Colorado potato beetle		
PS	Example 1; page -; 22pp; English.		
CC	Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning		
CC	mutagenesis of domain II of the CryIIIA protein of Bacillus		
CC	thuringiensis. All the positions changed to alanine in these proteins		
CC	are located in some of the solvent exposed loops and beta-strands		

CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.32 microgram per millilitre, compared to 2.88 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

xx Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIWPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIWPSEDPMKAFMEQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 QY 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLKLTQOET 240
 DB 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLKLTQOET 240
 QY 241 DHCVKYANGLDKLRSSYESWVNEFRYRREMTLYVLDAIFPLDYALYKREKTELT 300
 DB 241 DHCVKYANGLDKLRSSYESWVNEFRYRREMTLYVLDAIFPLDYALYKREKTELT 300
 QY 301 RDVLDPYGVNNLRGTYGTFNSIENYIRKPHLFYLRHQHTRPQPGYTGNDSEFNWS 360
 DB 301 RDVLDPYGVNNLRGTYGTFNSIENYIRKPHLFYLRHQHTRPQPGYTGNDSEFNWS 360
 QY 361 GNVSRRPSTIGSNDITTSFYGKSKSEPVQNLFEENGEXYRAVANNTLWPSAVYSGVT 420
 DB 361 GNVSRRPSTIGSNDITTSFYGKSKSEPVQNLFEENGEXYRAVANNTLWPSAVYSGVT 420
 QY 421 KVEFSQYNDQTEASTQYDTSKRNVAGVMSIDQLPETTDEPLEKGYSHQNLNVYMCFL 480
 DB 421 KVEFSQYNDQTEASTQYDTSKRNVAGVMSIDQLPETTDEPLEKGYSHQNLNVYMCFL 480
 QY 481 MGSRSRTIYLVLTTHKSVDFPNMIDSKKITQPLVYKAYLQSGASVVAAPRTGGIIOC 540
 DB 481 MGSRSRTIYLVLTTHKSVDFPNMIDSKKITQPLVYKAYLQSGASVVAAPRTGGIIOC 540
 QY 541 TENGSAATIVYPPDVYSOKYRARIHYASTSQTFTLSLDGAPFNQYDFDKTINKGDTLT 600
 DB 541 TENGSAATIVYPPDVYSOKYRARIHYASTSQTFTLSLDGAPFNQYDFDKTINKGDTLT 600
 QY 601 YNSFNLASFSTPELSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSTPELSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 33

AAW34827 ID AAW34827 standard; Protein; 644 AA.

xx AC AAW34827;

xx DT 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein S385A.

xx CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
 xx increased toxicity; Coleopteran insect; Colorado potato beetle;
 xx relative solvent accessibility; plant resistance;
 xx Diabrotica virgifera virgifera.

OS Synthetic.
 OS Bacillus thuringiensis.

FH Key Location/Qualifiers

FT MISC-difference 385

FT /label= S385A
 FT /note= "wild type Ser replaced with Ala"

PN US5659123-A.

PD 19-AUG-1997.

PE 26-AUG-1994; 94US-0295060.

PF 26-AUG-1994; 94US-0295060.

PR (PLB2) PLANT GENETIC SYSTEMS NV.

PI Janssens S, Peferoen M, Van Rie J;

PS WPI: 1997-424316/39.

PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

PS Example 1; Page -: 22pp; English.

xx Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 xx mutagenesis of domain II of the CryIIIA protein of Bacillus
 xx thuringiensis. All the positions changed to alanine in these proteins
 xx are located in some of the solvent exposed loops and beta-strands
 xx directed towards or located at the molecular apex. The substituted amino
 xx acids have a relative solvent accessibility of at least 40%, or are a
 xx maximum distance of 3 amino acids away from an amino acid having at least
 xx 40% relative solvent accessibility. The novel CryIIIA proteins have an
 xx increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 xx and can be used to combat, or improve plant resistance towards insects.
 xx Specifically, the toxicity of the present sequence towards Diabrotica
 xx virgifera virgifera was tested. The EC50 value (concentration at which
 xx 50% feeding inhibition is observed) of the present protein was found to
 xx be 0.78 microgram per millilitre, compared to 2.88 microgram per
 xx millilitre for the wild type CryIIIA protein.
 xx note: this sequence does not appear in the specification; it was created
 xx using information provided.

SO Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIWPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIWPSEDPMKAFMEQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 QY 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLKLTQOET 240
 DB 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLKLTQOET 240

```

Db 181 MPFAISGEVLEFLTTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
Qy 241 DHCWKYNNVGLDKRGSSYESWVNFNRYRREMTLVLDIALPPLVDVLYREKVTETLT 300
Db 241 DHCWKYNNVGLDKRGSSYESWVNFNRYRREMTLVLDIALPPLVDVLYREKVTETLT 300
Qy 301 RDVLTDPVGVNMLRGYGTTFSENIENYIRKPHLPDLHRIQFHTRPQPGYGNDSFNWMS 360
Db 301 RDVLTDPVGVNMLRGYGTTFSENIENYIRKPHLPDLHRIQFHTRPQPGYGNDSFNWMS 360
Qy 361 GNVYSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Db 361 GNVYSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Qy 421 KVEFSQYNDQTDASTQTIDSKRNVAWSIDQLPETTDEPLEKGSYHOLNVMCF 480
Db 421 KVEFSQYNDQTDASTQTIDSKRNVAWSIDQLPETTDEPLEKGSYHOLNVMCF 480
Qy 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIIC 540
Db 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIIC 540
Qy 541 TENGSAATIVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Db 541 TENGSAATIVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Qy 601 YNSFNLASFSSTPELPGNNLQIGVTGLSAGDKVYIDKIEFIIPVN 644
Db 601 YNSFNLASFSSTPELPGNNLQIGVTGLSAGDKVYIDKIEFIIPVN 644

RESULT 34
AAW34828
ID AAW34828 standard; Protein: 644 AA.
XX
AC AAW34828;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein V448A.
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Dldrotica virgifer a virgifer a.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FT Key Location/Qualifiers
FT MISC-difference 448 /label= "V448A"
FT /note= "wild type Val replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI; 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIIIA proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.

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XX
CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards diabrotica
CC virgifer a virgifer a was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 11.52 microgram per millilitre, compared to 4.04 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA;
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MNPNNRSEHDTIKTTENNEVPTNHNVOYPLAETPPTLEDLNYKEFLMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNEVPTNHNVOYPLAETPPTLEDLNYKEFLMTADNNTALDSS 60
Qy 61 TTKVDVIOKGISVVDLGLVGVGFPFGALVSFTYNTFLNTMPSDEDPKAFMEQVEALMDOK 120
Db 61 TTKVDVIOKGISVVDLGLVGVGFPFGALVSFTYNTFLNTMPSDEDPKAFMEQVEALMDOK 120
Qy 121 IADYAKKALAELOGLONNVEDYVYALSQKNPVSSRNPHSGGRITRELFQASHFRNS 180
Db 121 IADYAKKALAELOGLONNVEDYVYALSQKNPVSSRNPHSGGRITRELFQASHFRNS 180
Qy 181 MPFAISGEVLEFLTTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
Db 181 MPFAISGEVLEFLTTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
Qy 241 DHCWKYNNVGLDKRGSSYESWVNFNRYRREMTLVLDIALPPLVDVLYREKVTETLT 300
Db 241 DHCWKYNNVGLDKRGSSYESWVNFNRYRREMTLVLDIALPPLVDVLYREKVTETLT 300
Qy 301 RDVLTDPVGVNMLRGYGTTFSENIENYIRKPHLPDLHRIQFHTRPQPGYGNDSFNWMS 360
Db 301 RDVLTDPVGVNMLRGYGTTFSENIENYIRKPHLPDLHRIQFHTRPQPGYGNDSFNWMS 360
Qy 361 GNVYSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Db 361 GNVYSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
Qy 421 KVEFSQYNDQTDASTQTIDSKRNVAWSIDQLPETTDEPLEKGSYHOLNVMCF 480
Db 421 KVEFSQYNDQTDASTQTIDSKRNVAWSIDQLPETTDEPLEKGSYHOLNVMCF 480
Qy 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIIC 540
Db 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIIC 540
Qy 541 TENGSAATIVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Db 541 TENGSAATIVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Qy 601 YNSFNLASFSSTPELPGNNLQIGVTGLSAGDKVYIDKIEFIIPVN 644
Db 601 YNSFNLASFSSTPELPGNNLQIGVTGLSAGDKVYIDKIEFIIPVN 644

RESULT 35
AAW34829
ID AAW34829 standard; Protein: 644 AA.

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XX AC AAM34829;
XX DT 25-FEB-1998 (first entry)
XX DE Novel CryIIIA mutant protein S449A.
XX KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX KM increased toxicity; Coleopteran insect; Colorado potato beetle;
XX KM relative solvent accessibility; plant resistance;
XX KM Diabrotica virgifera virgifera.
XX OS Synthetic.
XX OS Bacillus thuringiensis.
XX FH Key Location/Qualifiers
XX FT Misc-difference 449 /label= S449A
XX FT /note= "wild type Ser replaced with Ala"
XX PN US5659123-A.
XX PD 19-AUG-1997.
XX PE 26-AUG-1994; 94US-0295060.
XX PR 26-AUG-1994; 94US-0295060.
XX PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX PI Jansens S, Peferoen M, Van Rie J;
XX DR WPI: 1997-424316/39.
XX PT Modified Bacillus thuringiensis CryIII proteins - with increased
XX PT toxicity against insect pests, particularly Coleopteran insects,
XX PT e.g. corn rootworm and Colorado potato beetle
XX PS Example 1; Page -: 22pp; English.
XX CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
XX CC mutagenesis of domain II of the CryIIIA protein of Bacillus
XX CC thuringiensis. All the positions changed to alanine in these proteins
XX CC are located in some of the solvent exposed loops and beta-strands
XX CC directed towards or located at the molecular apex. The substituted amino
XX CC acids have a relative solvent accessibility of at least 40%, or are a
XX CC maximum distance of 3 amino acids away from an amino acid having at least
XX CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX CC and can be used to combat, or improve plant resistance towards insects.
XX CC Specifically, the toxicity of the present sequence towards Diabrotica
XX CC virgifera virgifera was tested. The EC50 value (concentration at which
XX CC 50% feeding inhibition is observed) of the present protein was found to
XX CC be 7.12 microgram per millilitre, compared to 4.04 microgram per
XX CC millilitre for the wild type CryIIIA protein.
XX CC note: this sequence does not appear in the specification; it was created
XX CC using information provided.
XX CC
XX Sequence 644 AA:

```

```

Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 MNPNNSEHDTKTENNEPTNHYOYPLAETNPTELDNLYEFLRMDRDNTEALDSS 60
DB 1 MNPNNSEHDTKTENNEPTNHYOYPLAETNPTELDNLYEFLRMDRDNTEALDSS 60
OY 61 TTRDVIQKGISVVDLGVVGFPGALVSFTYNTLNTIPSEDPKAKMEQVEALMDOK 120
DB 61 TTRDVIQKGISVVDLGVVGFPGALVSFTYNTLNTIPSEDPKAKMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180

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DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
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DB 181 MFSFAISGTEVYFLTTYQAANTHLFLKDAQIYEEMKYEKEDIABEYKROKLTQDEYT 240
OY 241 DHCQKMYNGLKLGSSYESVWNNRYRREMTLVLDLALFPLYDRLVPKEKTELT 300
DB 241 DHCQKMYNGLKLGSSYESVWNNRYRREMTLVLDLALFPLYDRLVPKEKTELT 300
OY 301 RDVLTDPVIGVNNLRGSGTTFESNIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFNWYS 360
DB 301 RDVLTDPVIGVNNLRGSGTTFESNIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFNWYS 360
OY 361 GNVYSTRPSIGSNDITTSFFYGNKSSEPVQNLFEFNGEYVYRAVANTNLAVPSAVYSGVT 420
DB 361 GNVYSTRPSIGSNDITTSFFYGNKSSEPVQNLFEFNGEYVYRAVANTNLAVPSAVYSGVT 420
OY 421 KYEFSQYNDQTEASTQYTDSDKRNVGAVASWDSIDQLPETTDEPLEKGYSHOLNVWCFL 480
DB 421 KYEFSQYNDQTEASTQYTDSDKRNVGAVASWDSIDQLPETTDEPLEKGYSHOLNVWCFL 480
OY 481 MGSRGTLPLVLTWTHKSVDFEWMIDSKKITQLPLVKAYKLGASVAVGPRFTGGDIIOC 540
DB 481 MGSRGTLPLVLTWTHKSVDFEWMIDSKKITQLPLVKAYKLGASVAVGPRFTGGDIIOC 540
OY 541 TENGSAATITVYPPDVYSQKRYARIRHYASTOITTTLSLDGAPFQOYTFDXTKNGDPLT 600
DB 541 TENGSAATITVYPPDVYSQKRYARIRHYASTOITTTLSLDGAPFQOYTFDXTKNGDPLT 600
OY 601 YNSFNLASFSPTFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSPTFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

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RESULT 36
AAM34830
ID AAM34830 standard; Protein: 644 AA.
XX
XX

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AC AAM34830;
XX
XX DT 25-FEB-1998 (first entry)
XX DE Novel CryIIIA mutant protein G310A.

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KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KM increased toxicity; Coleopteran insect; Colorado potato beetle;
KM relative solvent accessibility; plant resistance;
KM Diabrotica virgifera virgifera.
OS Synthetic.
OS Bacillus thuringiensis.

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FH Key Location/Qualifiers
FT Misc-difference 310 /label= G310A
FT /note= "wild type Gly replaced with Ala"

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XX PN US5659123-A.
XX PD 19-AUG-1997.
XX PE 26-AUG-1994; 94US-0295060.
XX PR 26-AUG-1994; 94US-0295060.
XX PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX PI Jansens S, Peferoen M, Van Rie J;
XX WPI: 1997-424316/39.
XX

```



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OY 61 TTKDVIQGISVGGDLGVGFPFGALVSEYTNFLNTIMPSDEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQGISVGGDLGVGFPFGALVSEYTNFLNTIMPSDEDPKAFMEQVEALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDYVSSALSSQKNPSSNPNHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSSALSSQKNPSSNPNHSGRIRELFSQASHFRNS 180
OY 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
DB 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
OY 241 DHCVMYVNGDLKLGSSYSESWVNFRRREMTLVLDLALFPLYDRLYPKKTELT 300
DB 241 DHCVMYVNGDLKLGSSYSESWVNFRRREMTLVLDLALFPLYDRLYPKKTELT 300
OY 301 RDVLTDPVGVNMLRGYGTTFSSNIENYIRKPHLEFLYLRIOFHTRPOGYGNDSPFNYS 360
DB 301 RDVLTDPVGVNMLRGYGTTFSSNIENYIRKPHLEFLYLRIOFHTRPOGYGNDSPFNYS 360
OY 361 GNYVSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
OY 421 KVEFSQYNDQDEASTQYDYSKRNVAVSWDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
DB 421 KVEFSQYNDQDEASTQYDYSKRNVAVSWDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
OY 481 MGSRGITPVLWTWTHKSVDFFNMIDSKKITQPLVKAKKLGSGASVYAGPRTGGDIIOC 540
DB 481 MGSRGITPVLWTWTHKSVDFFNMIDSKKITQPLVKAKKLGSGASVYAGPRTGGDIIOC 540
OY 541 TENGAATITVYTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFEDTKINKGDTLT 600
DB 541 TENGAATITVYTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFEDTKINKGDTLT 600
OY 601 YNSFNLASFSPTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFTIPVN 644
DB 601 YNSFNLASFSPTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFTIPVN 644

RESULT 38
AAM34832
ID AAM34832 standard; Protein: 644 AA.
XX
AC AAM34832:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein L408A.
XX
KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT MISC-difference 408 /label= L408A
FT /note= "wild type Lau replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.

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```

XX Jansens S, Peferoen M, Van Rie J;
PI WPI: 1997-424316/39.
XX
DR Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 4.29 microgram per millilitre, compared to 3.08 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification: it was created
CC using information provided.
XX
SQ Sequence 644 AA:
XX
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MNPNNRSEHDTIKTTENNEVPJNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTTENNEVPJNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
OY 61 TTKDVIQGISVGGDLGVGFPFGALVSEYTNFLNTIMPSDEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQGISVGGDLGVGFPFGALVSEYTNFLNTIMPSDEDPKAFMEQVEALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDYVSSALSSQKNPSSNPNHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSSALSSQKNPSSNPNHSGRIRELFSQASHFRNS 180
OY 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
DB 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
OY 241 DHCVMYVNGDLKLGSSYSESWVNFRRREMTLVLDLALFPLYDRLYPKKTELT 300
DB 241 DHCVMYVNGDLKLGSSYSESWVNFRRREMTLVLDLALFPLYDRLYPKKTELT 300
OY 301 RDVLTDPVGVNMLRGYGTTFSSNIENYIRKPHLEFLYLRIOFHTRPOGYGNDSPFNYS 360
DB 301 RDVLTDPVGVNMLRGYGTTFSSNIENYIRKPHLEFLYLRIOFHTRPOGYGNDSPFNYS 360
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DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
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DB 421 KVEFSQYNDQDEASTQYDYSKRNVAVSWDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
OY 481 MGSRGITPVLWTWTHKSVDFFNMIDSKKITQPLVKAYKLGSGASVYAGPRTGGDIIOC 540
DB 481 MGSRGITPVLWTWTHKSVDFFNMIDSKKITQPLVKAYKLGSGASVYAGPRTGGDIIOC 540
OY 541 TENGAATITVYTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFEDTKINKGDTLT 600
DB 541 TENGAATITVYTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFEDTKINKGDTLT 600

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DB 541 TENGSAATITVTPDVSYQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 600
 QY 601 YNSFNLASFTPELSSGNNLQIGVGLSAGDKVYIDKIEFTIPVN 644
 DB 601 YNSFNLASFTPELSSGNNLQIGVGLSAGDKVYIDKIEFTIPVN 644

RESULT 39
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 ID AAM34833 standard; Protein: 644 AA.
 XX
 AC AAM34833;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein P348A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 348 /label= P348A
 FT /note= "wild type Pro replaced with Ala"
 XX
 US5659123-A.
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLBZ) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI: 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Claim 18; Page -: 22pp; English.
 XX
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 12.47 microgram per millilitre, compared to 3.08 microgram per
 CC millilitre for the wild type CryIIIA protein. This mutant protein is
 CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification. It was created
 CC using information provided.
 XX
 XX Sequence 644 AA:
 SQ

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEYPTNHVQYPLAETPNPLEDLNRYEELRMADNNTTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEYPTNHVQYPLAETPNPLEDLNRYEELRMADNNTTEALDSS 60
 QY 61 TTKDVIOKGISVYGDLLGVGPPFGALVSFYTNPLNTIPMSDDPKAFMEQVEALMDOK 120
 DB 61 TTKDVIOKGISVYGDLLGVGPPFGALVSFYTNPLNTIPMSDDPKAFMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNEDYVSALSSQKMPVSRNPHSGRIRELFSSQASHFRNS 180
 DB 121 IADYAKKALAELOGLONNEDYVSALSSQKMPVSRNPHSGRIRELFSSQASHFRNS 180
 QY 181 MPSPFAISGEVLEFLTYQAANTHLFLKDAQIYGEEMYEKEDIAEFYKROLKLTQEY 240
 DB 181 MPSPFAISGEVLEFLTYQAANTHLFLKDAQIYGEEMYEKEDIAEFYKROLKLTQEY 240
 QY 241 DHCYKMYNNGLDKRGSSYSWVNFNRYREMTLVLDLALFPLVDVRLYPREVKTETLT 300
 DB 241 DHCYKMYNNGLDKRGSSYSWVNFNRYREMTLVLDLALFPLVDVRLYPREVKTETLT 300
 QY 301 RDVLTDPYGVNMLRGYGTFFSNIENYIRKPHLEFDYLHRIQFHTRPQGYGNDSEFNYS 360
 DB 301 RDVLTDPYGVNMLRGYGTFFSNIENYIRKPHLEFDYLHRIQFHTRPQGYGNDSEFNYS 360
 QY 361 GNYVSTRPSIGSNDIITSPYGNKSSPPVONLENGEKYRAVANNTLWAPSAVYSGYT 420
 DB 361 GNYVSTRPSIGSNDIITSPYGNKSSPPVONLENGEKYRAVANNTLWAPSAVYSGYT 420
 QY 421 KVERSOYNNQDQDEASTQTYDSKRNVGAVSWDSIDOLPPEPTDDPLKGYSHOINYMCF 480
 DB 421 KVERSOYNNQDQDEASTQTYDSKRNVGAVSWDSIDOLPPEPTDDPLKGYSHOINYMCF 480
 QY 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQPLPVKAYKLGQASAVYAGBRTGDIIOC 540
 DB 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQPLPVKAYKLGQASAVYAGBRTGDIIOC 540
 QY 541 TENGSAATITVTPDVSYQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 600
 DB 541 TENGSAATITVTPDVSYQKRYRARIHYASTQITFTLLSDGAPFNQYFDKTIKNGDTLT 600
 QY 601 YNSFNLASFTPELSSGNNLQIGVGLSAGDKVYIDKIEFTIPVN 644
 DB 601 YNSFNLASFTPELSSGNNLQIGVGLSAGDKVYIDKIEFTIPVN 644

RESULT 40
 AAM34834
 ID AAM34834 standard; Protein: 644 AA.
 XX
 AC AAM34834;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein I376A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 376 /label= I376A
 FT /note= "wild type Ile replaced with Ala"
 XX
 XX Sequence 644 AA:
 PN US5659123-A.

CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

SO Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNPNNRSEHDTIKTTENNNEVPTNHQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTTENNNEVPTNHQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
OY 61 TTKDVIQKGISVYVGLDLYGVGPFEGALVSFTYNTLNTWPSDEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQKGISVYVGLDLYGVGPFEGALVSFTYNTLNTWPSDEDPKAFMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
OY 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEWGEKEDIAPFYKROLKLTQEXT 240
DB 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEWGEKEDIAPFYKROLKLTQEXT 240
OY 241 DHCVKWYVNGDLKLGSSYESSWVNNRYRRENTLVLDLALFPLYDRLPKKVKTELT 300
DB 241 DHCVKWYVNGDLKLGSSYESSWVNNRYRRENTLVLDLALFPLYDRLPKKVKTELT 300
OY 301 RDVLDPIYGVNNLKGTYTTSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
DB 301 RDVLDPIYGVNNLKGTYTTSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
OY 361 GNYVSTRPSIGSNDITTSPPYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDITTSPPYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420
OY 421 KVESQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPEETDEPLEKGYSHQLYVWCF 480
DB 421 KVESQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPEETDEPLEKGYSHQLYVWCF 480
OY 481 MOGSRTIPVLTWTHKSYDFNMDSKRTIQLPLVKAQKLGSGAVAGPFTGDIIOC 540
DB 481 MOGSRTIPVLTWTHKSYDFNMDSKRTIQLPLVKAQKLGSGAVAGPFTGDIIOC 540
OY 541 TENGSAATIVYTPDYVSQKRYARHIASTQITFTLSLDGAPNOYFFDKTINKGDTLT 600
DB 541 TENGSAATIVYTPDYVSQKRYARHIASTQITFTLSLDGAPNOYFFDKTINKGDTLT 600
OY 601 YNSFRLAEFTSTPPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFRLAEFTSTPPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 42
AAM34836
ID AAM34836 standard; Protein: 644 AA.
AC AAM34836;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein I375A.
XX
KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KM increased toxicity; Coleopteran insect; Colorado potato beetle;
KN relative solvent accessibility; plant resistance;
KN Diabrotica virgifera virgifera.
XX
OS Synthetic.
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers

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FT Misc-difference 375
FT /label= I375A
FT /note= "wild type Ile replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -; 22pp; English.
XX
XX Novel CryIIIA proteins AAM3481-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards insects.
XX Specifically, the toxicity of the present sequence towards Diabrotica
XX virgifera virgifera was tested. The EC50 value (concentration at which
XX 50% feeding inhibition is observed) of the present protein was found to
XX be 1.65 microgram per millilitre, compared to 0.95 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA:
XX
XX Query Match 84.3%; Score 543; DB 18; Length 644;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MNPNNRSEHDTIKTTENNNEVPTNHQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTTENNNEVPTNHQYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
OY 61 TTKDVIQKGISVYVGLDLYGVGPFEGALVSFTYNTLNTWPSDEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQKGISVYVGLDLYGVGPFEGALVSFTYNTLNTWPSDEDPKAFMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
OY 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEWGEKEDIAPFYKROLKLTQEXT 240
DB 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEWGEKEDIAPFYKROLKLTQEXT 240
OY 241 DHCVKWYVNGDLKLGSSYESSWVNNRYRRENTLVLDLALFPLYDRLPKKVKTELT 300
DB 241 DHCVKWYVNGDLKLGSSYESSWVNNRYRRENTLVLDLALFPLYDRLPKKVKTELT 300
OY 301 RDVLDPIYGVNNLKGTYTTSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
DB 301 RDVLDPIYGVNNLKGTYTTSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
OY 361 GNYVSTRPSIGSNDITTSPPYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420

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Db 361 GNYSTRPSISGNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVYSGVT 420
Qy 421 KVEFSQYNDQTDASTQYDYSKRNVAWSIDQLPPTTDEPLEKGYSHQNLVWMCFL 480
Db 421 KVEFSQYNDQTDASTQYDYSKRNVAWSIDQLPPTTDEPLEKGYSHQNLVWMCFL 480
Qy 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKLQSGASVYAGPRFTGGDIQC 540
Db 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKLQSGASVYAGPRFTGGDIQC 540
Qy 541 TENGSAATITVTPDVYSQYKRYRARIHYASTQITFTLSLDGAPFNQYEDTKINKGDTLT 600
Db 541 TENGSAATITVTPDVYSQYKRYRARIHYASTQITFTLSLDGAPFNQYEDTKINKGDTLT 600
Qy 601 YNSFNLASFSPTPELSGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLASFSPTPELSGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

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RESULT 43

AAW34837

ID AAW34837 standard; Protein: 644 AA.

AC AAW34837;

DT 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein Y416A.

XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;

KW increased toxicity; Coleopteran insect; Colorado potato beetle;

KW relative solvent accessibility; plant resistance;

KW Diabrotica virgifera virgifera.

OS Synthetic.

OS Bacillus thuringiensis.

FH Key location/Qualifiers

FT Misc-difference 416

FT /label- Y416A

FT /note- "wild type Tyr replaced with Ala"

XX US5659123-A.

XX 19-AUG-1997.

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

XX 26-AUG-1994;

Specifically, the toxicity of the present sequence towards *Diabrotica virgifera virgifera* was tested. The EC50 value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be >356 microgram per millilitre, compared to 3.82 microgram per millilitre for the wild type CryIIIA protein. This mutant protein is recognised as a "down mutant" for *Diabrotica virgifera virgifera*. The toxicity of the mutant protein for this *Diabrotica* pest was significantly below the toxicity of the native CryIIIA protein. CC note: this sequence does not appear in the specification; it was created using information provided.

SQ Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MNPNNRSEHDTIKTTENNEVPYTHVOYPLAETPNPLEDLNRYKEFLMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNEVPYTHVOYPLAETPNPLEDLNRYKEFLMTADNNTALDSS 60
Qy 61 TTKDVIQKISVYGDLLGVVGFPEFGALVSFTYNTPLNTIPSDPPKATPEQVEALMDOK 120
Db 61 TTKDVIQKISVYGDLLGVVGFPEFGALVSFTYNTPLNTIPSDPPKATPEQVEALMDOK 120
Qy 121 IADYAKKALAELOGLONNEDYVYALSQKPNVSRNPHSGRIRLEFSQASHFRNS 180
Db 121 IADYAKKALAELOGLONNEDYVYALSQKPNVSRNPHSGRIRLEFSQASHFRNS 180
Qy 181 MPSPASIGVEYELFTYYAQAANTHFLKDAQITGEMGEYKEDIAEFYKROKLQOXYT 240
Db 181 MPSPASIGVEYELFTYYAQAANTHFLKDAQITGEMGEYKEDIAEFYKROKLQOXYT 240
Qy 241 DHCYKMYNGLDKLRGSSYSWVNFNRYRREMTLYVDLALPPLVDVRYLREVEYTELT 300
Db 241 DHCYKMYNGLDKLRGSSYSWVNFNRYRREMTLYVDLALPPLVDVRYLREVEYTELT 300
Qy 301 RDVLTDPYGVNNLRGTYGTFNSNIENYIRKPHLEFDYLRIOFTRPOPGYGNDSFNYS 360
Db 301 RDVLTDPYGVNNLRGTYGTFNSNIENYIRKPHLEFDYLRIOFTRPOPGYGNDSFNYS 360
Qy 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVYSGVT 420
Qy 421 KVEFSQYNDQTDASTQYDYSKRNVAWSIDQLPPTTDEPLEKGYSHQNLVWMCFL 480
Db 421 KVEFSQYNDQTDASTQYDYSKRNVAWSIDQLPPTTDEPLEKGYSHQNLVWMCFL 480
Qy 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKLQSGASVYAGPRFTGGDIQC 540
Db 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKLQSGASVYAGPRFTGGDIQC 540
Qy 541 TENGSAATITVTPDVYSQYKRYRARIHYASTQITFTLSLDGAPFNQYEDTKINKGDTLT 600
Db 541 TENGSAATITVTPDVYSQYKRYRARIHYASTQITFTLSLDGAPFNQYEDTKINKGDTLT 600
Qy 601 YNSFNLASFSPTPELSGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLASFSPTPELSGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

```

XX Claim 9; Page -; 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning

XX mutagenesis of domain II of the CryIIIA protein of *Bacillus*

XX thuringiensis. All the positions changed to alanine in these proteins

XX are located in some of the solvent exposed loops and beta-strands

XX directed towards or located at the molecular apex. The substituted amino

XX acids have a relative solvent accessibility of at least 40%, or are a

XX maximum distance of 3 amino acids away from an amino acid having at least

40% relative solvent accessibility. The novel CryIIIA proteins have an

increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

and can be used to combat, or improve plant resistance towards insects.

CryIIIA gene; corn rootworm toxicity; CryIIIA protein;

KM increased toxicity: Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility: plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key
 FT Misc-difference 327
 FT /label= y327A
 FT /note= "wild type Trp replaced with Ala"
 PN US5659123-A.
 XX 19-AUG-1997.
 PD 26-AUG-1994: 94US-0295060.
 XX 26-AUG-1994: 94US-0295060.
 PR 26-AUG-1994: 94US-0295060.
 XX
 PA (PLBZ) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI: 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1; Page -: 22pp; English.
 XX
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 2.40 microgram per millilitre, compared to 3.82 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 CC Sequence 644 AA:
 SQ
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDTIKTTENNEVPNHNQVPLAETPNPTLEDLNKKEPLRTADNNTFALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPNHNQVPLAETPNPTLEDLNKKEPLRTADNNTFALDSS 60
 QY 61 TTKDVIQKGISVAGDGLGVGFPFGALVSFTYNFLNTIMPESEDPWKAFMQVEALMDOK 120
 DB 61 TTKDVIQKGISVAGDGLGVGFPFGALVSFTYNFLNTIMPESEDPWKAFMQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSRRNPSSQGRIRLFSQAESHFENS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSRRNPSSQGRIRLFSQAESHFENS 180
 QY 181 MPSFAISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIJAEFYKROLKTOEY 240
 DB 181 MPSFAISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIJAEFYKROLKTOEY 240
 QY 241 DHCWKNVNGDLKLGSSYESWVNNRYRREMTLTVDLIALFPLDYRLYPKEVKELT 300

DB 241 DHCWKNVNGDLKLGSSYESWVNNRYRREMTLTVDLIALFPLDYRLYPKEVKELT 300
 QY 301 RDVLTDPVGVNMLRGITTFSENIENTIRKPHLFDYLRHQFHTRPGYTGDSFNYMS 360
 DB 301 RDVLTDPVGVNMLRGITTFSENIENTIRKPHLFDYLRHQFHTRPGYTGDSFNYMS 360
 QY 361 GNYSTRPSIGSNDIITSPFGNKSSEPVONLENGEKYRAVANNTLAWPNAVISGVT 420
 DB 361 GNYSTRPSIGSNDIITSPFGNKSSEPVONLENGEKYRAVANNTLAWPNAVISGVT 420
 QY 421 KVEFSQYNDQDEASTQYDYSKRNWGAWSIDQLPPTTDEPLEKGSQOLNVMCFL 480
 DB 421 KVEFSQYNDQDEASTQYDYSKRNWGAWSIDQLPPTTDEPLEKGSQOLNVMCFL 480
 QY 481 MGSRGITPVLWTWTKHSVDFFNMIDSKKITQPLVKAAYKIQSGASVYAGPFTGGDIQC 540
 DB 481 MGSRGITPVLWTWTKHSVDFFNMIDSKKITQPLVKAAYKIQSGASVYAGPFTGGDIQC 540
 QY 541 TENGSAATIVYTPDVSYSSOKYRARIRHVASSTQFTLSLDCAPFNOYFEPKTIKNGDTLT 600
 DB 541 TENGSAATIVYTPDVSYSSOKYRARIRHVASSTQFTLSLDCAPFNOYFEPKTIKNGDTLT 600
 QY 601 YNSFNLFASFYFPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644
 DB 601 YNSFNLFASFYFPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644
 RESULT 45
 AAW34839 standard; Protein; 644 AA.
 AC AAW34839;
 XX
 DT 25-FEB-1998 (first entry)
 DE
 XX Novel CryIIIA mutant protein F346A.
 KM CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key
 FT Misc-difference 346
 FT /label= F346A
 FT /note= "wild type Phe replaced with Ala"
 PN US5659123-A.
 XX 19-AUG-1997.
 PD 26-AUG-1994: 94US-0295060.
 XX 26-AUG-1994: 94US-0295060.
 PR 26-AUG-1994: 94US-0295060.
 XX
 PA (PLBZ) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI: 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Claim 9; Page -: 22pp; English.
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus

CC thuringensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested, and the present mutant protein was
 CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

CC Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 OY 61 TTKVDYIQKGISVYGDLLGVGFPFGALVSFTYNTFLNTIMPSDEDPKAFMEQVEALMDOK 120
 DB 61 TTKVDYIQKGISVYGDLLGVGFPFGALVSFTYNTFLNTIMPSDEDPKAFMEQVEALMDOK 120
 OY 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPSSRNPHSOGRIREFSQAESHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPSSRNPHSOGRIREFSQAESHFRNS 180
 OY 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPSSRNPHSOGRIREFSQAESHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPSSRNPHSOGRIREFSQAESHFRNS 180
 OY 181 MPEFAISGEVEFLFTYQAANTHLFLKDAQIYGEEMGEKEDIAEFFKRLKLTQEXT 240
 DB 181 MPEFAISGEVEFLFTYQAANTHLFLKDAQIYGEEMGEKEDIAEFFKRLKLTQEXT 240
 OY 241 DHCWKRYNGLDKLKGSSYEVNVRNRRREMTLVLDLALFPIYDRLPKYKTELT 300
 DB 241 DHCWKRYNGLDKLKGSSYEVNVRNRRREMTLVLDLALFPIYDRLPKYKTELT 300
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 DB 241 DHCWKRYNGLDKLKGSSYEVNVRNRRREMTLVLDLALFPIYDRLPKYKTELT 300
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 DB 301 RDVLTPPIYGVNNLRGTYGTFSENIENYIRKPHLFYLRHIOFHTRFQGYGNDSEFNYS 360
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 DB 301 RDVLTPPIYGVNNLRGTYGTFSENIENYIRKPHLFYLRHIOFHTRFQGYGNDSEFNYS 360
 OY 361 GNVYSTRPSIGSNDITSPFYGNKSESPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
 DB 361 GNVYSTRPSIGSNDITSPFYGNKSESPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
 OY 421 KVEFSQYNDOTDASTQYTDSCRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLVWCEFL 480
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 OY 481 MOGSRGTIPVLWTHTKSVDFNNMIDSKKITQLPLVAKAYLQSGASVAVGPRRTGGDIIOC 540
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RESULT 46
 AAM34840
 ID AAM34840 standard; Protein: 644 AA.
 XX AAM34840:
 AC
 XX

DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein Q347A.
 XX
 KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH
 FT Key location/Qualifiers
 FT Misc-difference 347 /label= Q347A
 FT /note="wild type Gln replaced with Ala"

US5659123-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 XX Jansens S, Peferoen M, Van Rie J;
 XX WPI; 1997-424316/39.

Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

PS Claim 9; Page -: 22pp; English.

XX
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested, and the present mutant protein was
 CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 601 YNSFNLASFSSTPELSCGNNLQIGVYGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSSTPELSCGNNLQIGVYGLSAGDKVYIDKIEFIPVN 644

RESULT 47
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AC AAM34841:
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DT 25-FEB-1998 (first entry)
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XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 442 /label= "S442A"
FT /note= "Wild type Ser replaced with Ala"
XX
PN US5659123-A.
XX
PD 19-AUG-1997.
XX
PE 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
PI Jansens S, Peferoen M, Van Rie J;
XX
DR WPI; 1997-424316/39.
XX
PT Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
e.g. corn rootworm and Colorado potato beetle

```

XX Claim 9; Page -: 22pp; English.

PS Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning

CC mutagenesis of domain II of the CryIIIA protein of Bacillus

CC thuringiensis. All the positions changed to alanine in these proteins

CC are located in some of the solvent exposed loops and beta-strands

CC directed towards or located at the molecular apex. The substituted amino

CC acids have a relative solvent accessibility of at least 40%, or are a

CC maximum distance of 3 amino acids away from an amino acid having at least

CC 40% relative solvent accessibility. The novel CryIIIA proteins have an

CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

CC and can be used to combat, or improve plant resistance towards insects.

CC Specifically, the toxicity of the present sequence towards Diabrotica

CC virgifera virgifera was tested, and the present mutant protein was

CC found to be a "down mutant" for Diabrotica virgifera virgifera. The

CC toxicity of the mutant protein for this Diabrotica pest was

CC significantly below the toxicity of the native CryIIIA protein.

CC note: this sequence does not appear in the specification; it was created

CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNPNNRSEHDTIKTTENNEVPTNHVOYPLAETNPPTLEDLNTKEFLRMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTTENNEVPTNHVOYPLAETNPPTLEDLNTKEFLRMTADNNTALDSS 60
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DB 121 IADYAKKKALAEIQLGQNNVEDYVSALSSWQKRPVSSRRPHSGRIRELFSQAESHPNS 180
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DB 181 MFSFAISGYEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFPYKROLKLTQET 240
OY 241 DHCWKYNNVGLDKLRGSSYESVWNNRYRREMTLVLDLALFPLYDRLPKKEVTELT 300
DB 241 DHCWKYNNVGLDKLRGSSYESVWNNRYRREMTLVLDLALFPLYDRLPKKEVTELT 300
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DB 301 RQVLDPIYGVNNLRGYGTFEINENYIRKPHLDYLRHIOFHRFOPGTYGNDSEFNWMS 360
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DB 361 GNVYSTRPSIGSNDIITSPFYGNKSSSEPVQNLFEENGKEKYRAVANTNLAVWPSAVYSGVT 420
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DB 421 KVEFSQYNDQDEASTQTYDSKRNKAVGWSIDQLPETTDEPLEKGYSHQNLNVMCF 480
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DB 481 MGSRGITPVLWTWTKSVDFNMIDSKKITQLPLVKAYKLGSGASVAVAGPFTGDIIOC 540
OY 541 TENGAATITVTPDVYSQKRYARIRHYASTQITFTLLSDGAPFNQYFPDKTINKGDTLT 600
DB 541 TENGAATITVTPDVYSQKRYARIRHYASTQITFTLLSDGAPFNQYFPDKTINKGDTLT 600
OY 601 YNSFNLASFSSTPELSCGNNLQIGVYGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSSTPELSCGNNLQIGVYGLSAGDKVYIDKIEFIPVN 644

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Fri Jan 10 14:49:33 2003

us-09-943-692-2.olig.rag

Page 37

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:49 : Search time 16 Seconds

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	644	100.0	644	1 US-07-828-788A-4	Sequence 4, Appl
2	644	100.0	644	1 US-08-072-281-2	Sequence 2, Appl
3	644	100.0	644	1 US-08-295-060-2	Sequence 2, Appl
4	644	100.0	644	1 US-08-759-446-2	Sequence 2, Appl
5	644	100.0	644	4 US-09-027-998A-2	Sequence 2, Appl
6	644	100.0	644	5 PCT-US92-11337-4	Sequence 4, Appl
7	644	100.0	652	3 US-08-993-722A-113	Sequence 113, App
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ALIGNMENTS

RESULT 1
US-07-828-788A-4
Sequence 4, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSER: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
AMTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGERIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMADGEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
US-07-828-788A-4

Query Match 100.0%; Score 644; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
 US-08-072-281-2

; Sequence 2, Application US/08072281
 ; Patent No. 5495071
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischhoff, David A.
 ; APPLICANT: Fuchs, Roy L.
 ; APPLICANT: Lavrik, Paul B.
 ; APPLICANT: McPherson, Sylvia A.
 ; APPLICANT: Perlick, Frederick J.
 ; TITLE OF INVENTION: Insect Resistant Plants
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lawrence M. Lavin, Jr., Monsanto Co., BBAF
 ; STREET: 700 Chesterfield Parkway No. 5495071th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: United States of America
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/072.281
 ; FILING DATE: 19930604
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/523284
 ; FILING DATE: 14-MAY-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lavin Jr., Lawrence M.
 ; REGISTRATION NUMBER: 30,768
 ; REFERENCE/DOCKET NUMBER: 38-21(10629)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 537-7286
 ; TELEFAX: (314) 537-6047
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 644 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-072-281-2

Query Match 100.0%; Score 644; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 KVEFSQYNDQTDASQYTDKRNKNGAVSWDSIDQLPPTTDEPLEKGYSHQUNYWCFL 480
OY 481 MOGSRGTPVLTWTHKSVDFNMIDSKKITQPLVNAVKLQSGASVYAGPRTGGDIIOC 540
DB 481 MOGSRGTPVLTWTHKSVDFNMIDSKKITQPLVNAVKLQSGASVYAGPRTGGDIIOC 540
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RESULT 3

US-08-295-060-2
Sequence 2, Application US/08295060
Patent No. 5659123
GENERAL INFORMATION:
APPLICANT: VAN RIE, Jeroen
APPLICANT: JANSSEN, Stefan
APPLICANT: PERREOEN, Marinix
TITLE OF INVENTION: NEW DIABROTICA TOXINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,060
FILING DATE: 26-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-295-060-2

Query Match 100.0%; Score 644; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPNNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
DB 1 MNPNNRSEHDITKTENNEVPNNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
QY 61 TTKDVIQGISVVDLGVGFPFGALVSYTFNLTNPSEDPMKAFMEQVEALMDOK 120
DB 61 TTKDVIQGISVVDLGVGFPFGALVSYTFNLTNPSEDPMKAFMEQVEALMDOK 120
QY 121 INDYAKNNALALOGQNNVEDYVSALSSWQNPVSSRPHSGQRIREFSQAESHFRNS 180
DB 121 INDYAKNNALALOGQNNVEDYVSALSSWQNPVSSRPHSGQRIREFSQAESHFRNS 180
QY 181 MSPFALSGEVEFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
DB 181 MSPFALSGEVEFLTTYAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
QY 241 DHCVKMYNVGLDKLGRSSYESVNNRRYRREMTLVLDLIAFLPYDVLVYKFEVKTETLT 300
DB 241 DHCVKMYNVGLDKLGRSSYESVNNRRYRREMTLVLDLIAFLPYDVLVYKFEVKTETLT 300
QY 301 ROVLNDPIYGVNNLNGYGTFSNIENYIRKPHLFDYLRHIOFHTROPQYNDSPFNYS 360
DB 301 ROVLNDPIYGVNNLNGYGTFSNIENYIRKPHLFDYLRHIOFHTROPQYNDSPFNYS 360
QY 361 GNVSTRPSIGSNDITSPFYGNKSSPQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVSTRPSIGSNDITSPFYGNKSSPQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
QY 421 KVEFSQINDQTEASTQYTDKRNKVGAVSWDSIDQLPPTTDEPLEKISHQLNTVMCTL 480

DB 421 KVEFSQINDQTEASTQYTDKRNKVGAVSWDSIDQLPPTTDEPLEKISHQLNTVMCTL 480
QY 481 MOGSRGTIPPLTWTHKSYDFNNMIDSKKITQLPLVAYAYKLGASVAGVAPRTGGDIIOC 540
DB 481 MOGSRGTIPPLTWTHKSYDFNNMIDSKKITQLPLVAYAYKLGASVAGVAPRTGGDIIOC 540
QY 541 TENGSAATYVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDKTIKNGDTLT 600
DB 541 TENGSAATYVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDKTIKNGDTLT 600
QY 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPVN 644
DB 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 4
US-08-759-446-2
Sequence 2, Application US/08759446
Patent No. 5763241
GENERAL INFORMATION:
APPLICANT: Fischhoff, David A.
APPLICANT: Fuchs, Roy L.
APPLICANT: Lavrik, Paul B.
APPLICANT: McPherson, Sylvia A.
APPLICANT: Perlak, Frederick J.
TITLE OF INVENTION: Insect Resistant Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lawrence M. Lavlin, Jr., Monsanto Co., B84F
STREET: 700 Chesterfield Parkway No. 5763241n
CITY: St. Louis
STATE: Missouri
COUNTRY: United States of America
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,446
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/072,281
FILING DATE:
APPLICATION NUMBER: 08/072,281
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lavlin Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 38-21(10629)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-759-446-2

Query Match 100.0%; Score 644; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPNNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
DB 1 MNPNNRSEHDITKTENNEVPNNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTAALDSS 60
QY 61 TTKDVIQGISVVDLGVGFPFGALVSYTFNLTNPSEDPMKAFMEQVEALMDOK 120

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Db 61 TTKDVIQGISVGDLLGVGPFPGALVSFTNFLTIMPSEDPKAFMEQVBLMDOK 120
Qy 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFNS 180
Db 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFNS 180
Qy 181 MPSPALSGEVLFTTYYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQOY 240
Db 181 MPSPALSGEVLFTTYYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQOY 240
Qy 241 DHCKWYNVGLDKLGGSSYSEWVNFNRRREMTLTVLDLALFPLDYRLYPKEVKTELT 300
Db 241 DHCKWYNVGLDKLGGSSYSEWVNFNRRREMTLTVLDLALFPLDYRLYPKEVKTELT 300
Qy 301 RDVLTDPVGVNLRGCTFESNIENYIRKPHLFYLRHIOFHRFOPGYGNDSEFNWS 360
Db 301 RDVLTDPVGVNLRGCTFESNIENYIRKPHLFYLRHIOFHRFOPGYGNDSEFNWS 360
Qy 361 GNYVSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPASVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPASVYSGVT 420
Qy 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
Db 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
Qy 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVKAAYKQSGASVAVAGRFPGDIIQC 540
Db 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVKAAYKQSGASVAVAGRFPGDIIQC 540
Qy 541 TENGSAATVYTPDVYSOKYRARIHASTSQITFTLSLDGAPPNQYFDKTIKNGDTLT 600
Db 541 TENGSAATVYTPDVYSOKYRARIHASTSQITFTLSLDGAPPNQYFDKTIKNGDTLT 600
Qy 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKYIYDKIEFIYPN 644
Db 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKYIYDKIEFIYPN 644

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RESULT 5
US-09-027-998A-2
Sequence 2, Application US/09027998A
Patent No. 6284949
GENERAL INFORMATION:
APPLICANT: Fischhoff, David A
APPLICANT: Fuchs, Roy L
TITLE OF INVENTION: Insect Resistant Plants
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold White and Durkee
STREET: PO Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,998A
FILING DATE: 23-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
INFORMATION FOR SEQ ID NO: 2:

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SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-027-998A-2

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Query Match 100.0%; Score 644; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLANTKEFLPMADNTEALSS 60
Db 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLANTKEFLPMADNTEALSS 60
Qy 61 TTKDVIQGISVGDLLGVGPFPGALVSFTNFLTIMPSEDPKAFMEQVBLMDOK 120
Db 61 TTKDVIQGISVGDLLGVGPFPGALVSFTNFLTIMPSEDPKAFMEQVBLMDOK 120
Qy 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFNS 180
Db 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFNS 180
Qy 181 MPSPALSGEVLFTTYYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQOY 240
Db 181 MPSPALSGEVLFTTYYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQOY 240
Qy 241 DHCKWYNVGLDKLGGSSYSEWVNFNRRREMTLTVLDLALFPLDYRLYPKEVKTELT 300
Db 241 DHCKWYNVGLDKLGGSSYSEWVNFNRRREMTLTVLDLALFPLDYRLYPKEVKTELT 300
Qy 301 RDVLTDPVGVNLRGCTFESNIENYIRKPHLFYLRHIOFHRFOPGYGNDSEFNWS 360
Db 301 RDVLTDPVGVNLRGCTFESNIENYIRKPHLFYLRHIOFHRFOPGYGNDSEFNWS 360
Qy 361 GNYVSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPASVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVMPASVYSGVT 420
Qy 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
Db 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
Qy 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVKAAYKQSGASVAVAGRFPGDIIQC 540
Db 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVKAAYKQSGASVAVAGRFPGDIIQC 540
Qy 541 TENGSAATVYTPDVYSOKYRARIHASTSQITFTLSLDGAPPNQYFDKTIKNGDTLT 600
Db 541 TENGSAATVYTPDVYSOKYRARIHASTSQITFTLSLDGAPPNQYFDKTIKNGDTLT 600
Qy 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKYIYDKIEFIYPN 644
Db 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKYIYDKIEFIYPN 644

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RESULT 6
PCT-US92-11337-4
Sequence 4, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID R. SALIMANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
FILING DATE: 19921231
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGERIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
PCT-US92-11337-4

Query Match 100.0%; Score 644; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNSEHDTIKTTENNEVPNTNHVQPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
1 MNPNNSEHDTIKTTENNEVPNTNHVQPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
61 TTKDVIQKGISVVGDLGVGPPFGALVSFTYNTLNTIMPSEDPWKAEMEVEALMDOK 120
61 TTKDVIQKGISVVGDLGVGPPFGALVSFTYNTLNTIMPSEDPWKAEMEVEALMDOK 120
121 IADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNPHSOGRIRELFSSQAESHRMS 180
121 IADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNPHSOGRIRELFSSQAESHRMS 180
121 IADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNPHSOGRIRELFSSQAESHRMS 180
181 MPSPAIISGYEVLFTTYAQAANTHLLFKDAQIYGEEMGEKEDIAEFYRKOLKIQEYT 240
181 MPSPAIISGYEVLFTTYAQAANTHLLFKDAQIYGEEMGEKEDIAEFYRKOLKIQEYT 240
181 MPSPAIISGYEVLFTTYAQAANTHLLFKDAQIYGEEMGEKEDIAEFYRKOLKIQEYT 240
241 DHCKVKNVNGDLKRGSSYSWVNFNRYRREMTLVLDLALPFLYDRLVPREVKTELT 300
241 DHCKVKNVNGDLKRGSSYSWVNFNRYRREMTLVLDLALPFLYDRLVPREVKTELT 300
301 RDVLTDPVGVNNGKGTFFSNENTIRKPHLFDYLRHQFPHRPGGYGNDSEFYMS 360
301 RDVLTDPVGVNNGKGTFFSNENTIRKPHLFDYLRHQFPHRPGGYGNDSEFYMS 360
301 RDVLTDPVGVNNGKGTFFSNENTIRKPHLFDYLRHQFPHRPGGYGNDSEFYMS 360
361 GNYSTRPSIGSNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
361 GNYSTRPSIGSNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
421 KVEFSQYNDQDEASTQYTSKRNKAVSWDSIDQLPPEPTDEPLEKGYSHQLNLYVCF 480
421 KVEFSQYNDQDEASTQYTSKRNKAVSWDSIDQLPPEPTDEPLEKGYSHQLNLYVCF 480
481 MGSRGITPVLWTNHSVDPEFNMDSKKITQPLVYKAYKLGSGASVYAGRFPGDIIQC 540

|||||
481 MGSRGITPVLWTNHSVDPEFNMDSKKITQPLVYKAYKLGSGASVYAGRFPGDIIQC 540
541 TENGSAATITVYPDVYSQKYRARIHYASTSQITFTLSLDGAPFNOYFEDRTINKGDTLT 600
541 TENGSAATITVYPDVYSQKYRARIHYASTSQITFTLSLDGAPFNOYFEDRTINKGDTLT 600
601 YNSFNLASFTPELFGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
601 YNSFNLASFTPELFGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 7
US-08-996-441B-113
Sequence 113, Application US/08996441B
Patent No. 6023013
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MICO:151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/474-7577
TELEFAX: 512/418-3000
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-441B-113

Query Match 100.0%; Score 644; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNSEHDTIKTTENNEVPNTNHVQPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
9 MNPNNSEHDTIKTTENNEVPNTNHVQPLAETPNPTLEDLNTKEFLRMADNNTALDSS 68
61 TTKDVIQKGISVVGDLGVGPPFGALVSFTYNTLNTIMPSEDPWKAEMEVEALMDOK 120
69 TTKDVIQKGISVVGDLGVGPPFGALVSFTYNTLNTIMPSEDPWKAEMEVEALMDOK 128
121 IADYAKKALAELOGLONNVEDYVSAISSQKPNVSSRNPHSOGRIRELFSSQAESHRMS 180

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Db 129 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFQAESHPFRNS 188
QY 181 MPEFAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 189 MPEFAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 248
QY 241 DHCYKWNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVRLYPKKEVKTFLT 300
Db 249 DHCYKWNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVRLYPKKEVKTFLT 308
QY 301 RDVLTDPIVGVNNLRGCTTSPNENIYIRKPHLFDYLRHIOFHRPQDGYGNDSPFYMS 360
Db 309 RDVLTDPIVGVNNLRGCTTSPNENIYIRKPHLFDYLRHIOFHRPQDGYGNDSPFYMS 368
QY 361 GNVYSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTMLAVMPASVYSGVT 420
Db 369 GNVYSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTMLAVMPASVYSGVT 428
QY 421 KVEFSQYNDQTDASTQTYDSKRNKAVSMDSIDQLPETTDEPLEKGYSHQNLVYMCFL 480
Db 429 KVEFSQYNDQTDASTQTYDSKRNKAVSMDSIDQLPETTDEPLEKGYSHQNLVYMCFL 488
QY 481 MGSRGITPVLTWTHKSVDFENMDSKKITQPLVKAKYKLGSGASVAVAGPFTGGDIIOC 540
Db 489 MGSRGITPVLTWTHKSVDFENMDSKKITQPLVKAKYKLGSGASVAVAGPFTGGDIIOC 548
QY 541 TENGSAATITVTPDVYSQYRARIHVASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600
Db 549 TENGSAATITVTPDVYSQYRARIHVASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 608
QY 601 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 609 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKVYIDKIEFIPVN 652

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RESULT 8
US-08-993-722A-113
Sequence 113, Application US/08993722A
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terssch, Michael A.
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLLECTORAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993/722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MEOO:149
TELECOMMUNICATION INFORMATION:

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TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-722A-113
Query Match 100.0%; Score 644; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MNPNNSEDDITKTNNNEVPNNHVOYPLAETPNPTLEDNANKFRLMADNTEALSS 60
Db 9 MNPNNSEDDITKTNNNEVPNNHVOYPLAETPNPTLEDNANKFRLMADNTEALSS 68
QY 61 TTKDVIQKISVVGDLGIVGPEFGALVSFTNPLNTIWPSEDPKAFMEQVEALMDQK 120
Db 69 TTKDVIQKISVVGDLGIVGPEFGALVSFTNPLNTIWPSEDPKAFMEQVEALMDQK 128
QY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFQAESHPFRNS 180
Db 129 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFQAESHPFRNS 188
QY 181 MPEFAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 189 MPEFAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 248
QY 241 DHCYKWNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVRLYPKKEVKTFLT 300
Db 249 DHCYKWNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVRLYPKKEVKTFLT 308
QY 301 RDVLTDPIVGVNNLRGCTTSPNENIYIRKPHLFDYLRHIOFHRPQDGYGNDSPFYMS 360
Db 309 RDVLTDPIVGVNNLRGCTTSPNENIYIRKPHLFDYLRHIOFHRPQDGYGNDSPFYMS 368
QY 361 GNVYSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTMLAVMPASVYSGVT 420
Db 369 GNVYSTRPSIGSNDIITSPFYGNKSSBPVONLEFNGEKYRAVANNTMLAVMPASVYSGVT 428
QY 421 KVEFSQYNDQTDASTQTYDSKRNKAVSMDSIDQLPETTDEPLEKGYSHQNLVYMCFL 480
Db 429 KVEFSQYNDQTDASTQTYDSKRNKAVSMDSIDQLPETTDEPLEKGYSHQNLVYMCFL 488
QY 481 MGSRGITPVLTWTHKSVDFENMDSKKITQPLVKAKYKLGSGASVAVAGPFTGGDIIOC 540
Db 489 MGSRGITPVLTWTHKSVDFENMDSKKITQPLVKAKYKLGSGASVAVAGPFTGGDIIOC 548
QY 541 TENGSAATITVTPDVYSQYRARIHVASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600
Db 549 TENGSAATITVTPDVYSQYRARIHVASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 608
QY 601 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 609 YNSFNILASFSTPELSCNNLIQIGVTGLSAGDKVYIDKIEFIPVN 652

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RESULT 9
US-08-993-170A-113
Sequence 113, Application US/08993170A
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terssch, Michael A.
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO

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: TITLE OF INVENTION: COLEOPTERAN INSECTS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/993,170A
: FILING DATE: 18-DEC-1997
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MECO:002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
:
: INFORMATION FOR SEQ ID NO: 113:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 652 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
:
: us-08-993-170A-113
:
: Query Match 100.0%; Score 644; DB 3; Length 652;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPTLEDLNTYKEFLRMFTADNNTALDSS 60
: Db 9 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPTLEDLNTYKEFLRMFTADNNTALDSS 68
:
: Oy 61 TTKDVIQKGISVYDGLLVGVGPEFGALVSFTYTNPLNTIMPSEDPKMAFMEOVEALMDOK 120
: Db 69 TTKDVIQKGISVYDGLLVGVGPEFGALVSFTYTNPLNTIMPSEDPKMAFMEOVEALMDOK 128
:
: Oy 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIRELFSQAESHPFNS 180
: Db 129 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIRELFSQAESHPFNS 188
:
: Oy 181 MPFALSIGYEVLETTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 240
: Db 189 MPFALSIGYEVLETTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 248
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: Oy 241 DHCVKRYNYGDLKLGSSYEVSVNPNRYRREMTLVLDLALFPLDYRLPKREKTELT 300
: Db 249 DHCVKRYNYGDLKLGSSYEVSVNPNRYRREMTLVLDLALFPLDYRLPKREKTELT 308
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: Oy 301 RDVLTPPIYGVNNLNGYGTTFNSNIENYIRKPHLFYLRHQFHTRQPGYIGNDSFNWS 360
: Db 309 RDVLTPPIYGVNNLNGYGTTFNSNIENYIRKPHLFYLRHQFHTRQPGYIGNDSFNWS 368
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: Oy 361 GNVVSTRPSIGSDITTSFYGNKSEPEYONLEFNGEKYRAYAVANTNLAVMPSAVYSGVT 420
: Db 369 GNVVSTRPSIGSDITTSFYGNKSEPEYONLEFNGEKYRAYAVANTNLAVMPSAVYSGVT 428
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: Oy 421 KVEFSYONDOTDASTQYTDSCRKNVAGVMSIDQLPEPTDEPLEKGYSHQNLNVMCFL 480
: Db 429 KVEFSYONDOTDASTQYTDSCRKNVAGVMSIDQLPEPTDEPLEKGYSHQNLNVMCFL 488
:
: Oy 481 MGSRGITPVLWTHRSVDFENMIDSKKITTQLPLVKAIVLQSGASVYAGPRTGGDIIOC 540
: Db 489 MGSRGITPVLWTHRSVDFENMIDSKKITTQLPLVKAIVLQSGASVYAGPRTGGDIIOC 548

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: Oy 541 TENGSAATVYTPDVSYSQYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDTLT 600
: Db 549 TENGSAATVYTPDVSYSQYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDTLT 608
:
: Oy 601 YNSFNLASFTPELGSNNLQIGVTGLSAGDKYIDKIEFIYN 644
: Db 609 YNSFNLASFTPELGSNNLQIGVTGLSAGDKYIDKIEFIYN 652
:
: RESULT 10
: us-08-993-775B-113
: Sequence 113, Application US/08993775B
: Patent No. 6077824
:
: GENERAL INFORMATION:
: APPLICANT: English, Leigh H.
: APPLICANT: Bruscock, Susan M.
: APPLICANT: Malvar, Thomas M.
: APPLICANT: Bryson, James W.
: APPLICANT: Kulesza, Caroline A.
: APPLICANT: Walters, Frederick S.
: APPLICANT: Slatin, Stephen L.
: APPLICANT: Von Tersch, Michael A.
:
: TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF
: DELTA-ENDOTOXINS AGAINST INSECT PESTS
:
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/993,775B
: FILING DATE: 18-DEC-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MECO:150
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
:
: INFORMATION FOR SEQ ID NO: 113:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 652 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
:
: us-08-993-775B-113
:
: Query Match 100.0%; Score 644; DB 3; Length 652;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPTLEDLNTYKEFLRMFTADNNTALDSS 60
: Db 9 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPTLEDLNTYKEFLRMFTADNNTALDSS 68
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: Oy 61 TTKDVIQKGISVYDGLLVGVGPEFGALVSFTYTNPLNTIMPSEDPKMAFMEOVEALMDOK 120
: Db 69 TTKDVIQKGISVYDGLLVGVGPEFGALVSFTYTNPLNTIMPSEDPKMAFMEOVEALMDOK 128
:
: Oy 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIRELFSQAESHPFNS 180
: Db 129 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIRELFSQAESHPFNS 188
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: Oy 181 MPFALSIGYEVLETTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 240

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Db 189 MPSEIISGSEVLEFLTYAAQANTHLFLKDAQIAGEEMGEKEDIAEFYKROLKQEXT 248
QY 241 DHCYKAVNGLDKLRGSSYESVWVFNRYRREMLTVLDLALPLVDRLYREXVTELT 300
Db 249 DHCYKAVNGLDKLRGSSYESVWVFNRYRREMLTVLDLALPLVDRLYREXVTELT 308
QY 301 RDVLTPDIVGVNNLRGVTGTFESNIENYIRKPHLEFDYLRHQIFHTRPQGYGNDSPNYS 360
Db 309 RDVLTPDIVGVNNLRGVTGTFESNIENYIRKPHLEFDYLRHQIFHTRPQGYGNDSPNYS 368
QY 361 GNYVSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
Db 369 GNYVSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 428
QY 421 KVEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPEETDEPLEKGSYHOLNVMCL 480
Db 429 KVEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPEETDEPLEKGSYHOLNVMCL 488
QY 481 MGSRCITPVLWTHKSVDFNNMIDSKKITQLPLVYKAYKLGASVYAGPRFTGGDIQC 540
Db 489 MGSRCITPVLWTHKSVDFNNMIDSKKITQLPLVYKAYKLGASVYAGPRFTGGDIQC 548
QY 541 TENGSATIVTPDVSYSOQRARIHASTSOTITFLSDGAPFNOYFDDKTINKGDTLT 600
Db 549 TENGSATIVTPDVSYSOQRARIHASTSOTITFLSDGAPFNOYFDDKTINKGDTLT 608
QY 601 YNSFNLAISTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 609 YNSFNLAISTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 652

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RESULT 11

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US-08-704-966-2
; Sequence 2, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sallwanchik, Lloyd & Sallwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:

```

```

NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88ARD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-966-2

```

```

Query Match 92.7%; Score 597; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 48 MTADNTEALDSSTTDVYQKISVVDLGVYFPPGALVSFYTNFLNTWSEDPWK 107
Db 1 MTADNTEALDSSTTDVYQKISVVDLGVYFPPGALVSFYTNFLNTWSEDPWK 60
QY 108 AFMEQVEALMDOKIADYAKNKALAELOGLNNVEDYVSLSMCKNPNVSSRNPSQKIR 167
Db 61 AFMEQVEALMDOKIADYAKNKALAELOGLNNVEDYVSLSMCKNPNVSSRNPSQKIR 120
QY 168 ELFSQAESHFRRMSPEFSAISGEVLEFLTYAAQANTHLFLKDAQIAGEEMGEKEDIAE 227
Db 121 ELFSQAESHFRRMSPEFSAISGEVLEFLTYAAQANTHLFLKDAQIAGEEMGEKEDIAE 180
QY 228 FYKROLKTOEYTDHCYKYNVGLDKLRGSSYESVWVFNRYRREMLTVLDLALPLVD 287
Db 181 FYKROLKTOEYTDHCYKYNVGLDKLRGSSYESVWVFNRYRREMLTVLDLALPLVD 240
QY 288 VRLYREXVTELTLDPLVDPIGVNNLRGYGTFESNIENYIRKPHLEFDYLRHQIFHTRFQ 347
Db 241 VRLYREXVTELTLDPLVDPIGVNNLRGYGTFESNIENYIRKPHLEFDYLRHQIFHTRFQ 300
QY 348 PGYGGNDSPNYSGNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTN 407
Db 301 PGYGGNDSPNYSGNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTN 360
QY 408 LAVMPSAVYSGVTKEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPEETDEPLEK 467
Db 361 LAVMPSAVYSGVTKEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPEETDEPLEK 420
QY 468 GYSHOLNVMCLMGSRCITPVLWTHKSVDFNNMIDSKKITQLPLVYKAYKLGASVY 527
Db 421 GYSHOLNVMCLMGSRCITPVLWTHKSVDFNNMIDSKKITQLPLVYKAYKLGASVY 480
QY 528 AGPRFTGGDIQCTENGSAITIVTPDVSYSOQRARIHASTSOTITFLSDGAPFNOY 587
Db 481 AGPRFTGGDIQCTENGSAITIVTPDVSYSOQRARIHASTSOTITFLSDGAPFNOY 540
QY 588 YFDKTIKNGDTLTYNSFNLAISTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 541 YFDKTIKNGDTLTYNSFNLAISTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 597

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RESULT 12

```

US-08-705-438-2
; Sequence 2, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Salliwanchik, Lloyd & Salliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/705,438
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 597 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-705-438-2

Query Match 92.7%; Score 597; DB 3; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALDSSTTKDYIOKGISVGDLLGVGFFPGALVSYTFMLTIMPSDEPMK 107
 DB 1 MTADNNTALDSSTTKDYIOKGISVGDLLGVGFFPGALVSYTFMLTIMPSDEPMK 60
 QY 108 AFMEQVEALMDOKIADYAKNKALAELOGLQNNVEDYVSALSSMOKNPVSSRNPHSQRIR 167
 DB 61 AFMEQVEALMDOKIADYAKNKALAELOGLQNNVEDYVSALSSMOKNPVSSRNPHSQRIR 120
 QY 168 ELFSQASHFRNSMPSFALISGEVLFLLTYQAANTHLFLKDAQIYGEENGKEKEDIAE 227
 DB 121 ELFSQASHFRNSMPSFALISGEVLFLLTYQAANTHLFLKDAQIYGEENGKEKEDIAE 180
 QY 228 FFKROLKLTQETDHCVKMYNGLDKLGSSYESVWNNRRYRREMTLVLDLALFLPLYD 287
 DB 181 FFKROLKLTQETDHCVKMYNGLDKLGSSYESVWNNRRYRREMTLVLDLALFLPLYD 240
 QY 288 VRLYPRKVTETLRLVDLPDIYGVNNLKQYGTTFESNIENYIRKPHLEPYLHRIQFHRFQ 347
 DB 241 VRLYPRKVTETLRLVDLPDIYGVNNLKQYGTTFESNIENYIRKPHLEPYLHRIQFHRFQ 300
 QY 348 PGYGGDSFNYSNGVNSRPSISGNDITSPFYGNKSSEPQNLFEENGKRYRAVANTN 407
 DB 301 PGYGGDSFNYSNGVNSRPSISGNDITSPFYGNKSSEPQNLFEENGKRYRAVANTN 360
 QY 408 LAWPAVYSGVYKVEFSQYNDQTEASTQTYDSKRNVGAVSWSDIDLPEPTDEPLEK 467

DB 361 LAWPAVYSGVYKVEFSQYNDQTEASTQTYDSKRNVGAVSWSDIDLPEPTDEPLEK 420
 QY 468 GYSHQNLVWYCFMLOGSRGTIPVLTWTHKSVDFPMNIDSKITQPLVKAAYKLOGSASV 527
 DB 421 GYSHQNLVWYCFMLOGSRGTIPVLTWTHKSVDFPMNIDSKITQPLVKAAYKLOGSASV 480
 QY 528 AGPFTGGDIIOCTENGSAATIVYVDPVYSOKYRARIHYASTSOTITLSIDGAPFNOY 587
 DB 481 AGPFTGGDIIOCTENGSAATIVYVDPVYSOKYRARIHYASTSOTITLSIDGAPFNOY 540
 QY 588 YPDKTKKGDPLVYNSFNPLASFPELGGNNLQIGVGLSAGDVIYIDKIEFIPVN 644
 DB 541 YPDKTKKGDPLVYNSFNPLASFPELGGNNLQIGVGLSAGDVIYIDKIEFIPVN 597

RESULT 13
 US-08-704-966-4
 Sequence 4, Application US/08704966
 Patent No. 601523
 GENERAL INFORMATION:
 APPLICANT: Adang, Michael J.
 APPLICANT: Rocheleau, Thomas A.
 APPLICANT: Merlo, Donald
 APPLICANT: Murray, Elizabeth E.
 TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Salliwanchik, Lloyd & Salliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/704,966
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-704-966-4

Query Match 92.4%; Score 595; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSSTTKVDVIGKISVVDLGVGPFPGALVSEFTNPLNTIMPSEDPMKAF 109
 DB 3 ADNNTALDSSSTTKVDVIGKISVVDLGVGPFPGALVSEFTNPLNTIMPSEDPMKAF 62

QY 110 MEQVEALMDOKIADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSGRIREL 169
 DB 63 MEQVEALMDOKIADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSGRIREL 122

QY 170 FSOAESHRNSMPSFAISGEVLEFLTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 229
 DB 123 FSOAESHRNSMPSFAISGEVLEFLTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 182

QY 230 KRQLKLTQETDHCWKYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLYDVR 289
 DB 183 KRQLKLTQETDHCWKYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLYDVR 242

QY 290 LYPKVETELTRDVLDPDPIVGVNNLRGVTGTSNIENTYIRKPHLDYLRHIOFHTRFOPG 349
 DB 243 LYPKVETELTRDVLDPDPIVGVNNLRGVTGTSNIENTYIRKPHLDYLRHIOFHTRFOPG 302

QY 350 YGNDSPFNWMSGNYSTRPSIGSNDIITSPYGNKSEPEVONLEFNGEKYRAVANNTLA 409
 DB 303 YGNDSPFNWMSGNYSTRPSIGSNDIITSPYGNKSEPEVONLEFNGEKYRAVANNTLA 362

QY 410 VMPNAVYSGVTAKVEFSQYNDQDEASTQYDYSKRNVGAVSWSIDQLPETTDEPLEKGY 469
 DB 363 VMPNAVYSGVTAKVEFSQYNDQDEASTQYDYSKRNVGAVSWSIDQLPETTDEPLEKGY 422

QY 470 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKIKITQPLVYAKKIQSGASVYAG 529
 DB 423 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKIKITQPLVYAKKIQSGASVYAG 482

QY 530 PRFTGGDIIOCTENGSAATITVTPDVSYSQYRARIHYASTQITFTLSLDGAPNOYF 589
 DB 483 PRFTGGDIIOCTENGSAATITVTPDVSYSQYRARIHYASTQITFTLSLDGAPNOYF 542

QY 590 DKTINKGDTLTVNSFNLASFTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFIPVN 644
 DB 543 DKTINKGDTLTVNSFNLASFTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFIPVN 597

RESULT 14
 US-08-705-438-4
 ; Sequence 4, Application US/08705438
 ; Patent No. 6015891
 ; GENERAL INFORMATION:
 ; APPLICANT: Adang, Michael J.
 ; APPLICANT: Rochelleau, Thomas A.
 ; APPLICANT: Merlo, Donald
 ; APPLICANT: Murray, Elizabeth E.
 ; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
 ; TITLE OF INVENTION: Gene
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 ; STREET: 1000 Legion Place, Suite 1750
 ; CITY: Orlando
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32801
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,438
 ; FILING DATE: 29-AUG-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/369,839

FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFDA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 610 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 US-08-705-438-4

Query Match 92.4%; Score 595; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSSTTKVDVIGKISVVDLGVGPFPGALVSEFTNPLNTIMPSEDPMKAF 109
 DB 3 ADNNTALDSSSTTKVDVIGKISVVDLGVGPFPGALVSEFTNPLNTIMPSEDPMKAF 62

QY 110 MEQVEALMDOKIADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSGRIREL 169
 DB 63 MEQVEALMDOKIADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSGRIREL 122

QY 170 FSOAESHRNSMPSFAISGEVLEFLTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 229
 DB 123 FSOAESHRNSMPSFAISGEVLEFLTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 182

QY 230 KRQLKLTQETDHCWKYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLYDVR 289
 DB 183 KRQLKLTQETDHCWKYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLYDVR 242

QY 290 LYPKVETELTRDVLDPDPIVGVNNLRGVTGTSNIENTYIRKPHLDYLRHIOFHTRFOPG 349
 DB 243 LYPKVETELTRDVLDPDPIVGVNNLRGVTGTSNIENTYIRKPHLDYLRHIOFHTRFOPG 302

QY 350 YGNDSPFNWMSGNYSTRPSIGSNDIITSPYGNKSEPEVONLEFNGEKYRAVANNTLA 409
 DB 303 YGNDSPFNWMSGNYSTRPSIGSNDIITSPYGNKSEPEVONLEFNGEKYRAVANNTLA 362

QY 410 VMPNAVYSGVTAKVEFSQYNDQDEASTQYDYSKRNVGAVSWSIDQLPETTDEPLEKGY 469
 DB 363 VMPNAVYSGVTAKVEFSQYNDQDEASTQYDYSKRNVGAVSWSIDQLPETTDEPLEKGY 422

QY 470 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKIKITQPLVYAKKIQSGASVYAG 529
 DB 423 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKIKITQPLVYAKKIQSGASVYAG 482

QY 530 PRFTGGDIIOCTENGSAATITVTPDVSYSQYRARIHYASTQITFTLSLDGAPNOYF 589
 DB 483 PRFTGGDIIOCTENGSAATITVTPDVSYSQYRARIHYASTQITFTLSLDGAPNOYF 542

QY 590 DKTINKGDTLTVNSFNLASFTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFIPVN 644
 DB 543 DKTINKGDTLTVNSFNLASFTPELSSGNNLQIGVTGLSAGDKYVYIDKIEFIPVN 597

RESULT 15
 US-08-295-060-4

; Sequence 4, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jeroen
; APPLICANT: JANSSEN, Stefan
; APPLICANT: PEREROEN, Martin
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; US-08-295-060-4

Query Match 53.4%; Score 344; DB 1; Length 645;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NPNNSEHDTIKTENNEVPTNHVQPLAETPNPTLEDLNYKEFLRMTADNNTALDSST 61
DB 3 NPNNSEHDTIKTENNEVPTNHVQPLAETPNPTLEDLNYKEFLRMTADNNTALDSST 62
QY 62 TKDVIQKGISVVGDLGAVGPFPGALVSFTYNTLNTIWPSEDPKAFMEQVEALMDOKI 121
DB 63 TKDVIQKGISVVGDLGAVGPFPGALVSFTYNTLNTIWPSEDPKAFMEQVEALMDOKI 122
QY 122 ADYAKNKALAELOGLQNNVEDYVSALSSMOKNPVSSRNPHSGRIRELFSQASHFRNSM 181
DB 123 ADYAKNKALAELOGLQNNVEDYVSALSSMOKNPVSSRNPHSGRIRELFSQASHFRNSM 182
QY 182 PSFAISGEVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYTD 241
DB 183 PSFAISGEVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYTD 242
QY 242 HCVKKNVNGDLKRGSSYSVSVNFRNRYRREMTLVLDIALPPLYDVRLYPREVKTELTR 301
DB 243 HCVKKNVNGDLKRGSSYSVSVNFRNRYRREMTLVLDIALPPLYDVRLYPREVKTELTR 302
QY 302 DVLTPDIVGVNVLRGYGTFSNIENYIRKPHLFDYLHRIQFHTR 345
DB 303 DVLTPDIVGVNVLRGYGTFSNIENYIRKPHLFDYLHRIQFHTR 346

Search completed: January 10, 2003, 11:11:25
Job time : 17 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:09:35 : Search time 11 Seconds
(without alignments)
1135.844 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MNPNNRSEHDITKTENNNEV.....TGLSAGDKYIKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 118974 seqs, 19401057 residues

Word size: 0

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: Published Applications_AA:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	644	US-09-943-692-2	Sequence 2, Appl
2	20	3.1	20	US-09-943-692-3	Sequence 53, Appl
3	15	2.3	15	US-09-943-692-3	Sequence 3, Appl
4	12	1.9	12	US-09-943-692-47	Sequence 47, Appl
5	12	1.9	12	US-09-943-692-50	Sequence 50, Appl
6	11	1.7	11	US-09-943-692-26	Sequence 26, Appl
7	11	1.7	11	US-10-032-717-18	Sequence 8, Appl
8	10	1.6	673	US-10-032-717-18	Sequence 18, Appl
9	10	1.6	1210	US-10-032-717-4	Sequence 4, Appl
10	10	1.6	1316	US-10-120-544A-18	Sequence 4, Appl
11	10	1.6	1332	US-10-120-544A-6	Sequence 16, Appl
12	10	1.6	1386	US-10-120-544A-18	Sequence 6, Appl
13	9	1.4	9	US-09-738-363-31	Sequence 31, Appl
14	8	1.2	13	US-09-943-692-29	Sequence 29, Appl
15	8	1.2	16	US-09-943-692-20	Sequence 20, Appl
16	8	1.2	43	US-09-864-761-44452	Sequence 44452, A
17	7	1.1	64	US-09-796-692-1801	Sequence 1601, Ap
18	7	1.1	64	US-09-796-692-1801	Sequence 1801, Ap
19	7	1.1	64	US-09-796-692-2485	Sequence 2485, Ap

ALIGNMENTS

20	7	1.1	157	10	US-09-816-669A-2	Sequence 2, Appl
21	7	1.1	327	10	US-09-886-055-249	Sequence 249, App
22	7	1.1	485	9	US-09-712-363-208	Sequence 208, App
23	7	1.1	616	12	US-10-032-717-20	Sequence 20, Appl
24	7	1.1	617	12	US-10-032-717-34	Sequence 34, Appl
25	7	1.1	617	12	US-10-032-717-46	Sequence 46, Appl
26	7	1.1	620	12	US-10-032-717-30	Sequence 30, Appl
27	7	1.1	620	12	US-10-032-717-32	Sequence 32, Appl
28	7	1.1	620	12	US-10-032-717-42	Sequence 42, Appl
29	7	1.1	637	10	US-09-852-053-3	Sequence 3, Appl
30	7	1.1	643	10	US-09-826-660-25	Sequence 25, Appl
31	7	1.1	644	9	US-09-738-626-5330	Sequence 5330, Ap
32	7	1.1	667	12	US-10-032-717-6	Sequence 6, Appl
33	7	1.1	669	12	US-10-032-717-10	Sequence 10, Appl
34	7	1.1	669	12	US-10-032-717-16	Sequence 16, Appl
35	7	1.1	670	12	US-10-032-717-24	Sequence 24, Appl
36	7	1.1	670	12	US-10-032-717-44	Sequence 44, Appl
37	7	1.1	673	12	US-10-032-717-12	Sequence 12, Appl
38	7	1.1	673	12	US-10-032-717-22	Sequence 22, Appl
39	7	1.1	673	12	US-10-032-717-40	Sequence 40, Appl
40	7	1.1	673	12	US-10-032-717-40	Sequence 34, App
41	7	1.1	791	10	US-09-881-752A-334	Sequence 5208, Ap
42	7	1.1	892	9	US-09-738-626-5208	Sequence 4, Appl
43	7	1.1	1109	10	US-09-756-526A-4	Sequence 2, Appl
44	7	1.1	1163	10	US-09-756-526A-2	Sequence 23, Appl
45	7	1.1	1186	10	US-09-826-660-23	Sequence 2, Appl
			1206	12	US-10-032-717-2	

RESULT 1
US-09-943-692-2
Sequence 2, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAYRIK, PAUL B.
APPLICANT: McPHERSON, SYLVIA A.
APPLICANT: McPHERSON, FREDERICK J.
TITLE OF INVENTION: COLDOPEPERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195-1
CURRENT APPLICATION NUMBER: US/09/943, 692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027, 998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 644
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-2

Query Match
Best Local Similarity 100.0%; Score 644; DB 10; Length 644;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDITKTENNNEVPTNHQVPLAETPNTLEDLNYKFEKLRATADNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNNEVPTNHQVPLAETPNTLEDLNYKFEKLRATADNTEALDSS 60
QY 61 TTKDVYOKGIVSYGVDLGVYGFPGFALVSFTYNTFLNTIWPSEDFWAKFMQVEALNDOK 120
DB 61 TTKDVYOKGIVSYGVDLGVYGFPGFALVSFTYNTFLNTIWPSEDFWAKFMQVEALNDOK 120
QY 121 IADYAKKALAELOQIQNNVEDYVSLSSWQKNPPSSRRPHSGGRIRLFQSAESHFRNS 180
DB 121 IADYAKKALAELOQIQNNVEDYVSLSSWQKNPPSSRRPHSGGRIRLFQSAESHFRNS 180

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QY 101 MPEFAISGEVFLTTVAQAANTHLFLKDAQIGEMGEYKEDIAPFYKROKLTQERT 240
DB 101 MPEFAISGEVFLTTVAQAANTHLFLKDAQIGEMGEYKEDIAPFYKROKLTQERT 240
QY 241 DHCWAVYVWGDLKRGSSYESWVWENRYRREMTLYVDLALPFLYDVRLLYPAKVTETLT 300
DB 241 DHCWAVYVWGDLKRGSSYESWVWENRYRREMTLYVDLALPFLYDVRLLYPAKVTETLT 300
QY 301 RDVLTDPVGVNNLRGVTGTFESNIENYIRKPHLFDLHRIOPTRROPQYGDSTNYS 360
DB 301 RDVLTDPVGVNNLRGVTGTFESNIENYIRKPHLFDLHRIOPTRROPQYGDSTNYS 360
QY 361 GNYSTPISGNDITSPYGNKSEPVONLEFNGEKYRAVANTNLAVPSAVYSGYT 420
DB 361 GNYSTPISGNDITSPYGNKSEPVONLEFNGEKYRAVANTNLAVPSAVYSGYT 420
QY 421 KVEFSQYNDQTDASTQYTDKRNAGVAMSDSIDOLPPTTDEPLEKGYSHQNLVWCF 480
DB 421 KVEFSQYNDQTDASTQYTDKRNAGVAMSDSIDOLPPTTDEPLEKGYSHQNLVWCF 480
QY 481 MGSRGTPVLTWTHKSVYFNMIDSKATTQLPLVKAYKLGASGVAGPRTGGDIIOC 540
DB 481 MGSRGTPVLTWTHKSVYFNMIDSKATTQLPLVKAYKLGASGVAGPRTGGDIIOC 540
QY 541 TENGSAATYVTPDVYSQYRARIHYASTQITFTSLDAPFPNOYTFDKTINKGDTLT 600
DB 541 TENGSAATYVTPDVYSQYRARIHYASTQITFTSLDAPFPNOYTFDKTINKGDTLT 600
QY 601 YNSFNLASFPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644

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RESULT 2

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; Sequence 53, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-53

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Query Match 3.1%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 PNPTELDLVKKEPLRMTADN 52
DB 1 PNPTELDLVKKEFLRMTADN 20

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RESULT 3

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; Sequence 3, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.

```

```

; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-3

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Query Match 2.3%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDTIKTT 15
DB 1 MNPNNRSEHDTIKTT 15

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RESULT 4

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; Sequence 47, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-47

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Query Match 1.9%; Score 12; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPNNRSEHDTI 12
DB 1 MNPNNRSEHDTI 12

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RESULT 5

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; Sequence 50, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31

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PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 50
LENGTH: 12
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-943-692-50

Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 12;
Pred. No. 2.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 VYDKIEFIPVN 644
DB 1 VYDKIEFIPVN 12

RESULT 6
US-09-943-692-26
Sequence 26, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAVRIK, PAUL B.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERILAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT.195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-26

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 13;
Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSS 60
DB 3 ADNNTALDSS 13

RESULT 7
US-10-032-717-8
Sequence 8, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 667
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8

Query Match
Best Local Similarity 100.0%; Score 10; DB 12; Length 667;
Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 RREMTLVLD 278
DB 272 RREMTLVLD 281

RESULT 8
US-10-032-717-18
Sequence 18, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 673
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-18

Query Match
Best Local Similarity 100.0%; Score 10; DB 12; Length 673;
Pred. No. 0.098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 RREMTLVLD 278
DB 272 RREMTLVLD 281

RESULT 9
US-10-032-717-4
Sequence 4, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1210

TYPE: PRT
ORGANISM: *Bacillus thuringiensis*
US-10-032-717-4

Query Match
Best Local Similarity 1.6%; Score 10; DB 12; Length 1210;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 272 RREMTLVLD 281

RESULT 10

US-10-120-544A-4
Sequence 4, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP135
CURRENT APPLICATION NUMBER: US/10/120,544A
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 1316
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-4

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1316;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 297 RREMTLVLD 306

RESULT 11

US-10-120-544A-18
Sequence 18, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP135
CURRENT APPLICATION NUMBER: US/10/120,544A
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463

PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 1332
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-18

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1332;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 257 RREMTLVLD 266

RESULT 12

US-10-120-544A-6
Sequence 6, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP135
CURRENT APPLICATION NUMBER: US/10/120,544A
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 1386
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-6

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1386;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 298 RREMTLVLD 307

RESULT 13

US-09-738-363-31
Sequence 31, Application US/09738363
Patent No. US20010010932A1
GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
Schwab, George E.
Payne, Jewel M.
Narva, Kenneth E.
Foncerrada, Luis
TITLE OF INVENTION: Nematocidal Proteins
NUMBER OF SEQUENCE ADDRESSES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville

STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-738-363-31

Query Match 1.4%; Score 9; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 634 YIDKIEFIP 642
DB 1 YIDKIEFIP 9

RESULT 14
US-09-943-692-29
Sequence 29, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAVRIK, PAUL B.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-29

Query Match 1.2%; Score 8; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 LGVVGPF 84
DB 1 LGVVGPF 84

DB 2 LGVVGPF 9
RESULT 15
US-09-943-692-20
Sequence 20, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAVRIK, PAUL B.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-20

Query Match 1.2%; Score 8; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 633 YIDKIEF 640
DB 1 YIDKIEF 8

Search completed: January 10, 2003, 11:11:43
Job time : 12 secs

1.
2.

1.
2.

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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:29 ; Search time 21 Seconds
(without alignments)
2948.122 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MPNNRSEHDTKTENNENY.....TGLSNGDKYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR_73:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	652	2 A27323	parasporal crystal
2	644	100.0	652	1 JH0261	parasporal crystal
3	23	3.6	649	1 J39811	parasporal crystal
4	21	3.3	652	2 S10228	parasporal crystal
5	11	1.7	934	2 B28388	parasporal crystal
6	9	1.4	1157	1 S49247	parasporal crystal
7	8	1.2	260	2 A70248	hypothetical prote
8	8	1.2	329	2 D97340	DNA replication pr
9	8	1.2	357	2 AC2045	6-phosphofructokin
10	8	1.2	375	2 E75542	probable endogluc
11	8	1.2	483	2 T36811	probable integral
12	8	1.2	760	2 T24521	hypothetical prote
13	8	1.2	1138	2 A48944	parasporal crystal
14	8	1.2	1154	2 S39536	parasporal crystal
15	8	1.2	1156	2 S19306	parasporal crystal
16	57	1.1	57	2 H90881	hypothetical prote
17	57	1.1	57	2 A85737	hypothetical prote
18	89	1.1	89	2 A11499	hypothetical prote
19	130	1.1	130	2 T14749	hypothetical prote
20	133	1.1	133	2 T47132	translation initia
21	135	1.1	135	2 B69103	hypothetical prote
22	140	1.1	140	2 AC1280	hypothetical prote
23	140	1.1	140	2 AC1643	hypothetical prote
24	143	1.1	143	2 S23255	TSC-22 protein - m
25	144	1.1	144	2 JC4813	TGF beta-stimulate
26	162	1.1	162	2 T36328	probable secreted
27	194	1.1	194	2 AH0480	probable membrane
28	197	1.1	197	2 C70519	hypothetical prote
29	217	1.1	217	2 G84045	transcription regu

30	7	1.1	224	2 C82973	hypothetical prote
31	7	1.1	225	2 F87528	hypothetical prote
32	7	1.1	227	2 F70529	probable trka prot
33	7	1.1	227	2 G69491	conserved hypothet
34	7	1.1	230	2 T06309	glutathione peroxi
35	7	1.1	233	2 A69004	CDPdiacylglycerol-
36	7	1.1	233	2 C75290	hypothetical prote
37	7	1.1	243	2 C86758	hypothetical prote
38	7	1.1	259	2 E84125	hydroxylase BH3805
39	7	1.1	251	2 S53090	CD40 ligand - bov1
40	7	1.1	265	2 J00435	arcelin-1 seed pro
41	7	1.1	265	2 A40111	probable sugar apt
42	7	1.1	275	2 A95971	amino acid ABC tra
43	7	1.1	277	2 G71849	glutamine ABC tran
44	7	1.1	277	2 D64666	galactoside transp
45	7	1.1	288	2 AE3632	

ALIGNMENTS

RESULT 1

A27323 parasporal crystal protein crystal - Bacillus thuringiensis

N:Alternate names: coleopteran-specific insect control protein; crystal protein cryc;
C:Species: Bacillus thuringiensis
C:Date: 19-Nov-1988 #sequence, revision 19-Nov-1988 #ext, change 01-Dec-2000

C:Accession: A27323; A26053; A29987; A28407; S60781; I39812; I39813

C:Herrnstadt, C.; Gilroy, T.E.; Sobleski, D.A.; Bennett, B.D.; Gaertner, F.H.

Gene 57, 37-46, 1987

A:Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active

A:Reference number: A27323; MUID:88112860; PMID:2828180

A:Accession: A27323

A:Molecule type: DNA

A:Residues: 1-652 <HER>

A:Experimental source: strain San Diego

R:Hoeltje, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.

Nucleic Acids Res. 15, 7183, 1987

A:Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus t

A:Reference number: A26853; MUID:88015559; PMID:3658680

A:Accession: A26853

A:Molecule type: DNA

A:Residues: 9-652 <HOE>

A:Cross-references: GB:Y00420; NID:940252; PIDN:CAA68482.1; PID:940253

A:Experimental source: var. tenebrionis

R:McPherson, S.A.; Perlek, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff,

Bio/Technology 6, 61-66, 1988

A:Title: Characterization of the coleopteran-specific protein gene of Bacillus thurin

A:Reference number: A29987

A:Accession: A29987

A:Molecule type: DNA

A:Residues: 9-652 <SEK>

A:Experimental source: var. tenebrionis

R:Adams, L.F.; Mathews, S.; O'Hara, P.; Petersen, A.; Guertler, H.

Mol. Microbiol. 14, 381-389, 1994

A:Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized stra

A:Reference number: S60781; MUID:95131759; PMID:7830581

A:Accession: S60781

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 9-652 <ADA>

A:Cross-references: EMBL:U10985; NID:9506182; PIDN:AAC43266.1; PID:9514312

A:Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R.Wu, S.J.; Dean, D.H.
 J. Mol. Biol. 255, 628-640, 1996
 A:Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis
 A:Reference number: S62317; MUID:96163559; PMID:8568902
 A:Contents: annotation
 R:Donovan, W.P.; Gonzalez, J.M.
 Mol. Gen. Genet. 214, 365-372, 1988
 A:Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis
 A:Accession number: I39812; MUID:89112139; PMID:3146015
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 9-652 <RES>
 A:Cross-references: GB:M37207; MUID:9142735; PIDN:AAA50255.1; PID:g142736
 A:Experimental source: strain EG2158
 J. Teixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.
 J. Bacteriol. 175, 2952-2960, 1993
 A:Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a
 A:Reference number: I39813; MUID:9355939; PMID:8491716
 A:Accession: I39813
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 9-58 <RES>
 A:Cross-references: GB:I03393; MUID:9304150; PIDN:AAA22350.1; PID:g551698
 A:Gene: cryIIIA
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 100.0%; Score 644; DB 2; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNRSEHDTKTENNEVPNNHQPPLAETPNPTLEDLYNKEFLRMTADNNTLEALDSS 60
 DB 9 MNPNNRSEHDTKTENNEVPNNHQPPLAETPNPTLEDLYNKEFLRMTADNNTLEALDSS 68
 61 TTKDVIQGISVVGDLGVGPFPGALVSPTNFTNTPMSSEDPKMAFEQVEALMDOK 120
 DB 69 TTKDVIQGISVVGDLGVGPFPGALVSPTNFTNTPMSSEDPKMAFEQVEALMDOK 128
 121 IADYAKNKALELOGLQNNVEDYVSALSSWQKNPVSSRNPHSOGRIRELSQAESHPRNS 180
 DB 129 IADYAKNKALELOGLQNNVEDYVSALSSWQKNPVSSRNPHSOGRIRELSQAESHPRNS 188
 181 MPFAISGEVLFITTYAQAANTHLFLKDAQITGEEMGEKEDIKAEFYKRLKLTQERT 240
 DB 189 MPFAISGEVLFITTYAQAANTHLFLKDAQITGEEMGEKEDIKAEFYKRLKLTQERT 248
 241 DHCKWNVGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
 DB 249 DHCKWNVGDLKRGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 308
 301 RDVLTDPVGVNRLRGYGTFSNENYIRKPHLEFDYLRHQFTTRQPGTYGNDSEFNWS 360
 DB 309 RDVLTDPVGVNRLRGYGTFSNENYIRKPHLEFDYLRHQFTTRQPGTYGNDSEFNWS 368
 361 GNYVSTSPSGSNDITSPFYGNKSSPVONLEFNGEKYRAVANNTNLVMSAVYSGYT 420
 DB 369 GNYVSTSPSGSNDITSPFYGNKSSPVONLEFNGEKYRAVANNTNLVMSAVYSGYT 428
 421 KVEFSQYNDOTDEASTQTYDSKRNVGAVSWDSIDQLPEPTTDEPLEKYSQOLNVKCF 480
 DB 429 KVEFSQYNDOTDEASTQTYDSKRNVGAVSWDSIDQLPEPTTDEPLEKYSQOLNVKCF 488
 481 MGSRCRTIPVLTWTHKSVDFNNIDSKITQPLVKAAYLQSGAVVAGPRTGGDITQC 540
 DB 489 MGSRCRTIPVLTWTHKSVDFNNIDSKITQPLVKAAYLQSGAVVAGPRTGGDITQC 548
 541 TENGSAATYVPPDVSYSOKYRARIHYASTSQITFTLSLDGAPFNQYFEDTKNGDTLT 600
 DB 549 TENGSAATYVPPDVSYSOKYRARIHYASTSQITFTLSLDGAPFNQYFEDTKNGDTLT 608

QY 601 YNSFNLSFSTPELSEGNNTQIGVTGLSAGDKYIDKIEPIVN 644
 DB 609 YNSFNLSFSTPELSEGNNTQIGVTGLSAGDKYIDKIEPIVN 652

RESULT 2

JH0261
 parasporal crystal protein cry3Ca1 - Bacillus thuringiensis subsp. kurstaki (strain B
 N:Alternate names: parasporal crystal protein cryIIID
 C:Species: Bacillus thuringiensis subsp. kurstaki
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 01-Dec-2000
 C:Accession: JH0261; S18944
 R:Lambert, B.; Theunis, W.; Ayuda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Se
 Gene 110, 131-132, 1992
 A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crys
 A:Reference number: JH0261; MUID:92184108; PMID:1544571
 A:Accession: JH0261
 A:Molecule type: DNA
 A:Residues: 1-649 <LAMP>
 A:Cross-references: EMBL:X59797; MUID:940287; PIDN:CAA42469.1; PID:g40288
 C:Gene: cryIIID
 C:Superfamily: parasporal crystal protein

Query Match 3.6%; Score 23; DB 1; Length 649;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

139811
 parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
 N:Alternate names: parasporal crystal protein cryIIIB2
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence-revision 19-Jul-1996 #text-change 01-Dec-2000
 C:Accession: I39811
 R:Donovan, W.P.; Ruper, M.T.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson,
 Appl. Environ. Microbiol. 58, 3921-3927, 1992
 A:Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal c
 A:Reference number: I39811; MUID:93119147; PMID:1476436
 A:Accession: I39811
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-652 <RES>
 A:Cross-references: GB:M89794; MUID:9142729; PIDN:AAA22334.1; PID:g142730
 C:Gene: cryIIIB2
 C:Superfamily: parasporal crystal protein

Query Match 3.3%; Score 21; DB 2; Length 652;
 Best Local Similarity 100.0%; Pred. No. 3, 3e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 RIRELFSQASHFRNMPSPA 185
 DB 166 RIRELFSQASHFRNMPSPA 186

RESULT 4

S10228
 parasporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
 N:Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
 C:Species: Bacillus thuringiensis
 C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 01-Dec-2000
 C:Accession: S10228
 R:Stick, A.; Gaertner, F.; Wong, A.
 Nucleic Acids Res. 18, 1305, 1990
 A:Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of
 A:Reference number: S10228; MUID:90206811; PMID:2320431

A:Accession: S10228
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-659 <SIC>
 A:Cross-references: EMBL:X17123; NID:940258; PIDN:CAA34983.1; PID:940259
 C:Genetics:
 A:Gene: cryIIIB
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin; toxin

Query Match 3.3%; Score 21; DB 2; Length 659;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 RIRLFQASHFRNMPSTRA 185
 ||||||||||||||||||
 DB 174 RIRLFQASHFRNMPSTRA 194

RESULT 5
 B29838
 parasporal crystal protein - *Bacillus thuringiensis* subsp. *israelensis* (fragment)
 C:Species: *Bacillus thuringiensis* subsp. *israelensis*
 C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 01-Dec-2000
 C:Accession: B29838
 R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.
 J. Bacteriol. 166, 801-811, 1986
 A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticide
 A:Reference number: A94672; MUID:86223796; PMID:3011746
 A:Accession: B29838
 A:Molecule type: DNA
 A:Residues: 1-934 <TRHO>
 A:Cross-references: GB:M2662; NID:q143228
 C:Superfamily: parasporal crystal protein

Query Match 1.7%; Score 11; DB 2; Length 934;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 271 EMTLVLDLIA 281
 ||||||||||||
 DB 284 EMTLVLDLIA 294

RESULT 6
 S49247
 parasporal crystal protein cry9cal [validated] - *Bacillus thuringiensis*
 N:Alternate names: parasporal crystal protein cryIH
 C:Species: *Bacillus thuringiensis*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 C:Accession: A59350; S49247
 R:Ramberg, B.; Buyse, L.; Decock, C.; Janssens, S.; Plans, C.; Saey, B.; Seurlinck, J.; V.
 Appl. Environ. Microbiol. 62, 80-86, 1996
 A:Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity against
 A:Reference number: A59350; MUID:96141404; PMID:8572715
 A:Accession: A59350
 A:Molecule type: DNA
 A:Residues: 1-1157 <LAM>
 A:Cross-references: EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:9547556
 A:Experimental source: serovar toluworthi
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.4%; Score 9; DB 1; Length 1157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 ITQLPLVKA 517
 |||||||||
 DB 515 ITQLPLVKA 523

RESULT 7
 A70248
 hypothetical protein BBJ24 - Lyme disease spirochete plasmid J/1p38
 C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
 C:Accession: A70248

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh.
 son, D.; Peterson, J.; Kervatage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yu
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: A70248

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-260 <KLE>
 A:Cross-references: GB:AE000767; NID:92690175; PIDN:MAC66120.1; PID:92690212; TIGR:BB
 A:Experimental source: strain B31
 C:Genetics:
 A:Genome: plasmid

Query Match 1.2%; Score 8; DB 2; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 632 KYIDKIE 639
 |||||||
 DB 22 KYIDKIE 29

RESULT 8
 D97340
 DNA replication protein DnaC [imported] - *Clostridium acetobutylicum*
 C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: D97340
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4836, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97340
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-329 <KUR>
 A:Cross-references: GB:AE001437; PIDN:MAK81511.1; PID:q15026685; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC3588

Query Match 1.2%; Score 8; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 PNPTLEDL 40
 |||||||
 DB 235 PNPTLEDL 242

RESULT 9
 AC2045
 6-phosphofructokinase [imported] - *Nostoc* sp. (strain PCC 7120)
 C:Species: *Nostoc* sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AC2045
 R:Kaneh, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriju
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC2045

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA073612.1; PID:g17131003; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: att1913
 C:Superfamily: 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 1.2%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 592 TINKGDTL 599
 |||||||
 DB 77 TINKGDTL 84

RESULT 10
 E75542
 Probable endoglucanase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: E75542
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 266, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75542
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-375 <KMT>
 A:Cross-references: GB:AE00186; GB:AE000513; NID:g6457921; PIDN:AAF09817.1; PID:g645790
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0229
 A:Map position: 1
 C:Superfamily: thermophilic aminopeptidase I alpha chain

Query Match 1.2%; Score 8; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GDLLGVG 81
 |||||||
 DB 132 GDLLGVG 139

RESULT 11
 T36811

probable integral membrane transport protein - *Streptomyces coelicolor*
 C:Species: *Streptomyces coelicolor*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36811
 R:Olliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rønjandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21614
 A:Accession: T36811
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <OLIT>
 A:Cross-references: EMBL:AL096811; PIDN:CA046808.1; GSPDB:GN00070; SCODEB:SCI30A.31C
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCODEB:SCI30A.31C

Query Match 1.2%; Score 8; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 576 TSLSDGAP 583

DB 205 TSLSDGAP 212
 |||||||

RESULT 12
 T24521

hypothetical protein T05E11.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T24521
 R:Kershaw, J.

submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19903
 A:Accession: T24521
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-760 <WIL>
 A:Cross-references: EMBL:Z68751; PIDN:CA092973.1; GSPDB:GN00022; CESP:T05E11.3
 A:Experimental source: clone T05E11
 C:Genetics:
 A:Gene: CESP:T05E11.3
 A:Map position: 4
 A:Insertions: 16/1; 39/2; 378/3; 570/3
 C:Superfamily: heat shock protein 90

Query Match 1.2%; Score 8; DB 2; Length 760;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 188 GYEVFLPT 195
 |||||||
 DB 539 GYEVFLPT 546

RESULT 13
 A48944

paraspore crystal protein cry7na1 - *Bacillus thuringiensis*
 N:Alternate names: paraspore crystal protein cryIIIC
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
 C:Accession: A48944
 R:Lambert, B.; Holte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.

Appl. Environ. Microbiol. 58, 2536-2542, 1992
 A:Title: Novel *Bacillus thuringiensis* insecticidal crystal protein with a silent acti
 A:Reference number: A48944; MUID:92384571; PMID:1514800
 A:Contents: B7S1377
 A:Accession: A48944
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-1138 <LAM>
 A:Cross-references: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
 A:Note: sequence extracted from NCBI backbone (NCBI:112092, NCBI:112093)
 C:Superfamily: paraspore crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1138;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 451 DSIQDLP 458
 |||||||
 DB 438 DSIQDLP 445

RESULT 14
 S39536

paraspore crystal protein cry9ba1 - *Bacillus thuringiensis*
 N:Alternate names: delta-endotoxin-related protein; paraspore crystal protein cryX
 C:Species: *Bacillus thuringiensis*
 C:Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
 C:Accession: S39536
 R:Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Ste
 FEBS Lett. 336, 79-82, 1993

A:Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bacillus thuringiensis
 A:Reference number: S39536; MUID:94085596; PMID:8262221
 A:Accession: S39536
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1154 <SHE>
 A:Cross-references: EMBL:X75019
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1154;
 Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 ITQPLVVK 516
 |||||
 DB 517 ITQPLVVK 524

RESULT 15

S19306

parasporal crystal protein cry9Aa1 - Bacillus thuringiensis

N:Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal protein

C:Species: Bacillus thuringiensis

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000

C:Accession: S19306; S23588; A44847; S14602; S14837

R:Smulevitch, S.V.; Osterman, A.L.; Shevelov, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrc

FEBS Lett. 293, 25-28, 1991

A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIc of Bacillus thuringiensis

A:Reference number: S19306; MUID:92070568; PMID:1660003

A:Accession: S19306

A:Molecule type: DNA

A:Residues: 1-1156 <SMU>

A:Cross-references: EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:940271

A:Experimental source: subsp. galleriae

A:Accession: S23588

A:Molecule type: Protein

A:Residues: 24-34 <SMU1>

A:Experimental source: subsp. galleriae

R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.

J. gen. Microbiol. 138, 55-62, 1992

A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis

A:Reference number: A44847; MUID:92211329; PMID:156556

A:Accession: A44847

A:Molecule type: DNA

A>Status: preliminary

A:Cross-references: EMBL:X58534; NID:948879; PIDN:CAA41425.1; PID:948880

A:Experimental source: isolate DSIR517

A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBI:92867)

C:Genetics:

A:Gene: cryIG

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1156;
 Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 RYRREMTL 274
 |||||
 DB 267 RYRREMTL 274

Search completed: January 10, 2003, 11:11:04
 Job time : 24 secs

100

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:07:39 ; Search time 14 Seconds
(without alignments)
1907.911 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MNPNNRSEHDITKTENNEV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	644	1	C3AA_BACTT
2	23	3.6	649	1	C3CA_BACTK
3	21	3.3	652	1	C3BB_BACTU
4	21	3.3	659	1	C3BA_BACTU
5	17	2.6	648	1	C3AA_BACTJ
6	11	1.7	675	1	C3AA_BACTI
7	11	1.7	675	1	C3AA_BACTJ
8	10	1.6	682	1	C3BA_BACTH
9	10	1.6	1169	1	C8BA_BACTK
10	10	1.6	1169	1	C9DA_BACTP
11	9	1.4	674	1	C9AA_BACTP
12	9	1.4	1157	1	C9AA_BACTO
13	9	1.4	1157	1	C9CA_BACTO
14	8	1.2	618	1	CHAA_CLOBI
15	8	1.2	1138	1	C7AA_BACTU
16	8	1.2	1138	1	C7AB_BACTU
17	8	1.2	1138	1	C7AB_BACTK
18	8	1.2	1156	1	C9AA_BACTG
19	7	1.1	82	1	ATPH_OCHNE
20	7	1.1	134	1	ATPH_OCHNE
21	7	1.1	134	1	ATPH_OCHNE
22	7	1.1	135	1	ATPH_OCHNE
23	7	1.1	137	1	ATPH_OCHNE
24	7	1.1	143	1	ATPH_OCHNE
25	7	1.1	144	1	ATPH_OCHNE
26	7	1.1	157	1	ATPH_OCHNE
27	7	1.1	157	1	ATPH_OCHNE
28	7	1.1	201	1	ATPH_OCHNE
29	7	1.1	261	1	ATPH_OCHNE
30	7	1.1	265	1	ATPH_OCHNE
31	7	1.1	265	1	ATPH_OCHNE
32	7	1.1	327	1	ATPH_OCHNE
33	7	1.1	327	1	ATPH_OCHNE

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	AA
34	C3AA_BACTT	1	1	1	YETK_BACSU
35	C3AA_BACTT	1	1	1	CHAA_ECOLI
36	C3AA_BACTT	1	1	1	SUCC_PASMU
37	C3AA_BACTT	1	1	1	PRYC_SULSO
38	C3AA_BACTT	1	1	1	Y360_MYCGE
39	C3AA_BACTT	1	1	1	PHAL_PSELE
40	C3AA_BACTT	1	1	1	DCDA_METH
41	C3AA_BACTT	1	1	1	YBDA_BACSU
42	C3AA_BACTT	1	1	1	IRX2_MOUSE
43	C3AA_BACTT	1	1	1	UD18_RAT
44	C3AA_BACTT	1	1	1	AMAL_PLAFR
45	C3AA_BACTT	1	1	1	PK66_PLAKU
34	C3AA_BACTT	1	1	1	031540 bacillus su
35	C3AA_BACTT	1	1	1	P31801 escherichia
36	C3AA_BACTT	1	1	1	O9CND0 pasteurella
37	C3AA_BACTT	1	1	1	O9UX05 sulfolobus
38	C3AA_BACTT	1	1	1	O49426 mycoplasma
39	C3AA_BACTT	1	1	1	P52090 pseudomonas
40	C3AA_BACTT	1	1	1	O27390 methanobact
41	C3AA_BACTT	1	1	1	P39584 bacillus su
42	C3AA_BACTT	1	1	1	P81066 mus musculu
43	C3AA_BACTT	1	1	1	O64634 ratius norv
44	C3AA_BACTT	1	1	1	P22623 plasmodium
45	C3AA_BACTT	1	1	1	P21303 plasmodium
AC	P07130; P21255;	STANDARD;	PRT;	644	AA.
DT	01-APR-1988 (Rel. 07, Created)				
DT	01-APR-1988 (Rel. 07, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Pesticidal crystal protein cry3Aa precursor (insecticidal delta-				
DE	endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa				
DE	crystal protein).				
GN	CRY3AA OR CRYIIIA(A) OR CRYIIIA OR CRYC OR CRYC OR B13.				
OS	Bacillus thuringiensis (subsp. tenebrionis),				
OS	Bacillus thuringiensis (subsp. morrisoni), and				
OS	Bacillus thuringiensis (subsp. san diego).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI TaxID=1444, 1441, 1435;				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis;				
RC	MEDLINE=88015559; Pubmed=3658680;				
RA	Hoeft H., Seurinck J., Houtven A.V., Vaack M.;				
RT	"Nucleotide sequence of a gene encoding an insecticidal protein of				
RT	Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";				
RL	Nucleic Acids Res. 15:7183-7183(1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis;				
RC	McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavyk P.B.,				
RA	Fischhoff D.A.;				
RT	"Characterization of the coleopteran-specific protein gene of Bacillus				
RT	thuringiensis var. tenebrionis.";				
RL	Biotechnology 6:61-66(1988).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis; STRAIN=NB176;				
RC	MEDLINE=95131759; Pubmed=7830581;				
RA	Adams L.F., Mathews S., O'Hara P., Petersen A., Gurtler H.;				
RT	"Elucidation of the mechanism of CryIIIA overproduction in a				
RT	mutagenized strain of Bacillus thuringiensis var. tenebrionis.";				
RL	Mol. Microbiol. 14:381-389(1994).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis; STRAIN=EG2158;				
RC	MEDLINE=89112139; Pubmed=3146015;				
RA	Donovan W.P., Gonzalez J.M. Jr., Gilbert M.P., Dankosik C.C.;				
RT	"Isolation and characterization of EG2158, a new strain of Bacillus				
RT	thuringiensis toxic to coleopteran larvae, and nucleotide sequence of				
RT	the toxin gene.";				
RL	Mol. Gen. Genet. 214:365-372(1988).				

```

RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES-B.t.san diego;
RX MEDLINE-88112860; Pubmed-2828180;
RA Herrnstadt C., Gilroy T.E., Sobleski D.A., Bennett B.D.,
RA Gaertner P.H.;
RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
RT active delta-endotoxin gene from Bacillus thuringiensis subsp. san
RT diego.";
RL Gene 57:37-46(1987).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC SPECIES-B.t.tenebrionis;
RX MEDLINE-92049729; Pubmed-1658659;
RA Li J., Carroll J., Ellar D.J.;
RT Crystal structure of insecticidal delta-endotoxin from Bacillus
RT thuringiensis at 2.5-A resolution.";
RL Nature 353:815-821(1991).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOKULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- BIOCHEMISTRY: Introduced by genetic manipulation and expressed in
CC insect-resistant potato by Monsanto.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL: Y00420; CAA68482.1; -
DR EMBL: J02978; AAA22541.1; -
DR EMBL: M37207; AAA50255.1; -
DR EMBL: U10985; AAC43366.1; -
DR EMBL: M30503; AAA22542.1; -
DR EMBL: M22472; AAA22336.1; ALT_INT.
DR PIR: A26853; A26853.
DR PIR: A28407; A28407.
DR PIR: A29987; A29987.
DR PIR: A27323; A27323.
DR PDB: 1DLC; 30-SEP-94.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation; 3D-structure; Genetically modified food.
FT PROPEP 1 57 REMOVED IN NATURE FORM.
FT CHAIN 58 644 PESTICIDIAL CRYSTAL PROTEIN CRY3AA.
FT CONFLICT 544 544 G->A (IN REF. 3).
SO SEQUENCE 644 AA; 73108 MW; EFCEFLCEEFDA9683 CRC64;

```

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Query Match 100.0%; Score 644; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 MPSPALSGYEVLEFLTYAQAANTHFLKDAQIYGEWCEKEDIAEFKRRLKLTQET 240
QY 241 DHCKWYNVGLDKRGSSYSWVFNRYRREMTLYLDIALFPYLDVRLYKEVKTET 300
DB 241 DHCKWYNVGLDKRGSSYSWVFNRYRREMTLYLDIALFPYLDVRLYKEVKTET 300
QY 301 RDVLTDPVGVNMLRGYGFNSNIENYIRKPHLFDVLRHIOFTHFFOGYGNDSFNYS 360
DB 301 RDVLTDPVGVNMLRGYGFNSNIENYIRKPHLFDVLRHIOFTHFFOGYGNDSFNYS 360
QY 361 GNVYSTRPSIGSDITSPYGNKSEPOVNEFNKEKYRAVANTNLAVPSAYSGVT 420
DB 361 GNVYSTRPSIGSDITSPYGNKSEPOVNEFNKEKYRAVANTNLAVPSAYSGVT 420
QY 421 KVEFSQNDQDEASQYDYSQKRYARHVAHQITPTLSLDGAPRQYFDKTIKGDIT 480
DB 421 KVEFSQNDQDEASQYDYSQKRYARHVAHQITPTLSLDGAPRQYFDKTIKGDIT 480
QY 481 MOGSRGTIPVLTWTHKSVDFENKIDSKITQLPLVKAAYKLGASVAVGPRFTGDIIC 540
DB 481 MOGSRGTIPVLTWTHKSVDFENKIDSKITQLPLVKAAYKLGASVAVGPRFTGDIIC 540
QY 541 TENGSAATITVPDYSQKRYARHVAHQITPTLSLDGAPRQYFDKTIKGDIT 600
DB 541 TENGSAATITVPDYSQKRYARHVAHQITPTLSLDGAPRQYFDKTIKGDIT 600
QY 601 YNSFNLSFSTPELGSNNLQIGVTLSAGDKVYIDKIEFIPV 644
DB 601 YNSFNLSFSTPELGSNNLQIGVTLSAGDKVYIDKIEFIPV 644

RESULT 2
C3CA_BACTK STANDARD: PRT; 649 AA.
ID C3CA_BACTK
AC 045744;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cry3ca (insecticidal delta-endotoxin
DE CryIIIC(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
DE protein).
CN CRY3CA OR CRYIIIC(A) OR CRYIIID.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_taxid=29339;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN-BT1109P;
RA MEDLINE-92184108; Pubmed-1544571;
RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,
RA Jansens S., Seurinck J., Peferoen M.;
RT "Nucleotide sequence of gene cryIIID encoding a novel coleopteran-
RT active crystal protein from strain BT1109P of Bacillus thuringiensis
RT subsp. kurstaki.";
RL Gene 110:131-132(1992).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOKULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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DR EMBL: X59797; CAA42469.1; -
 DR HSSP: P07130; IDIC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 DR Toxin: Sporulation.
 KW SEQUENCE 649 AA; 73026 MW; 8FP1F0B47957AC49 CRC64;

Query Match 3.6%; Score 23; DB 1; Length 649;
 Best Local Similarity 100.0%; Pred. No. 4,7e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 GYGTFESNIENYIRKPHLEFDYLH 338
 Db 314 GYGTFESNIENYIRKPHLEFDYLH 336

RESULT 3
 C3BB_BACTU STANDARD; PRT; 652 AA.

ID C3BB_BACTU 006117; 045717;
 AC 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry3Bb (insecticidal delta-endotoxin
 DE CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa crystal
 DE protein).
 GN CRY3BB OR CRYIIIB(B) OR CRYIIIB2.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EG4961;
 RX MEDLINE=93119147; PubMed=1476436;
 RA Donovan W.P., Ruper M.J., Stanley A.C., Malvar T., Gawron-Burke M.C.,
 RA Johnson T.B.;
 RT "Characterization of two genes encoding Bacillus thuringiensis
 RT insecticidal crystal proteins toxic to Coleoptera species.";
 RL Appl. Environ. Microbiol. 58:3921-3927(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRL B-1655 / EG5144;
 RA Donovan W.P., Ruper M.J., Stanley A.C.;
 RT "Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran
 RT insects.";
 RL Patent number US5378625, 03-JAN-1995.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA. HAS MODERATE LEVEL OF TOXICITY TO
 CC SOUTHERN CORN ROOTWORM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 DR EMBL: M89794; AAA2334.1; -
 DR EMBL: U31633; AAA74198.1; -
 DR HSSP: P07130; IDIC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 DR Toxin: Sporulation.
 KW VARIANT 21 21 Q -> P (IN STRAIN EG5144).
 FT VARIANT 97 97 N -> D (IN STRAIN EG5144).
 FT VARIANT 97 97

FT VARIANT 289 289 I -> V (IN STRAIN EG5144).
 FT VARIANT 352 352 F -> S (IN STRAIN EG5144).
 FT VARIANT 417 419 YTL -> IYF (IN STRAIN EG5144).
 FT VARIANT 451 451 S -> G (IN STRAIN EG5144).
 FT VARIANT 590 590 L -> I (IN STRAIN EG5144).
 FT VARIANT 600 600 K -> I (IN STRAIN EG5144).
 FT VARIANT 624 624 K -> T (IN STRAIN EG5144).
 FT VARIANT 624 624
 KW SEQUENCE 652 AA; 74385 MW; 63048332CDE8CC6 CRC64;

Query Match 3.3%; Score 21; DB 1; Length 652;
 Best Local Similarity 100.0%; Pred. No. 5,2e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 RIRELFSQASHFRNSMPSPA 185
 Db 166 RIRELFSQASHFRNSMPSPA 186

RESULT 4
 C3BA_BACTO STANDARD; PRT; 659 AA.

ID C3BA_BACTO 017969;
 AC 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry3Ba (insecticidal delta-endotoxin
 DE CryIIIB(a)) (Crystalline entomocidal protoxin) (75 kDa crystal
 DE protein).
 GN CRY3BA OR CRYIIIB(A) OR CRYIIIB.
 OS Bacillus thuringiensis (subsp. tolworthi).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1442;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=43F;
 RX MEDLINE=90206811; PubMed=2320431;
 RA Sick A., Gaertner F.H., Wong A.;
 RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
 RT isolate of Bacillus thuringiensis subsp. tolworthi.";
 RL Nucleic Acids Res. 18:1305-1305(1990).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X17123; CAA34983.1; -
 DR EMBL: A07234; CAN00645.1; -
 DR PIR: S10228; S10228.
 DR HSSP: P07130; IDIC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 DR Toxin: Sporulation.
 KW SEQUENCE 659 AA; 75159 MW; 5A5B214FF84168CA CRC64;

Query Match 3.3%; Score 21; DB 1; Length 659;
 Best Local Similarity 100.0%; Pred. No. 5,2e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 RIRELFSQASHFRNSMPSPA 185
 Db 174 RIRELFSQASHFRNSMPSPA 194

RESULT 5
CJMA_BACTU STANDARD; PRT; 648 AA.
AC 032307;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cry19a (insecticidal delta-endotoxin protein) (CRY19A) (Crystaline entomocidal protoxin) (75 kDa crystal protein).
GN CRY19A OR CRY19A(A).
OS *Bacillus thuringiensis* (subsp. *jegasethesan*).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=56955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=367;
RX MEDLINE=98027382; PubMed=9361431;
RA Roso M.L., Delecluse A.;
RT "Contribution of the 65-kilodalton protein encoded by the cloned gene cry19a to the mosquitoicidal activity of *Bacillus thuringiensis* subsp. *jegasethesan*.";
RT Jegasethesan, J.;
RL Appl. Environ. Microbiol. 63:4449-4455(1997).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF MOSQUITOS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC -----
DR EMBL: Y07603; CAA68875.1; -.
DR HSP: P07130; IDLC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 648 AA; 74742 MW; E4ABFBA4570DE5B9 CRC64;
Query Match 2.6%; Score 17; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 262 WYENRYRREMTLVLD 278
DB 267 WYENRYRREMTLVLD 283

RESULT 6
CAAA_BACTI STANDARD; PRT; 675 AA.
AC P09662;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry10a (insecticidal delta-endotoxin protein) (CRY10A) (Crystaline entomocidal protoxin) (78 kDa crystal protein).
GN CRY10A OR CRY10A(A) OR CRY10C.
OS *Bacillus thuringiensis* (subsp. *israelensis*).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ONR60A;
RX MEDLINE=86223796; PubMed=3011746;
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,
RA Walfield A.M., Pollock T.J.;
RT "Structural similarity between the lepidoptera- and diptera-specific insecticidal endotoxin genes of *Bacillus thuringiensis* subsp. *jegasethesan*.";
RT J. Bacteriol. 166:801-811(1986).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF MOSQUITOS. ACTIVE ON ADIES AEGYPTI.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC -----
DR EMBL: M12662; AAA22614.1; -.
DR PIR: B29838; B29838.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 675 AA; 77760 MW; 2A70011BEA7985F5 CRC64;
Query Match 1.7%; Score 11; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 271 EMTLVLDLIA 281
DB 284 EMTLVLDLIA 294

RESULT 7
CPAA_BACTU STANDARD; PRT; 675 AA.
AC O87906;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry25a (insecticidal delta-endotoxin protein) (CRY25A) (Crystaline entomocidal protoxin) (76 kDa crystal protein).
GN CRY25A OR CRY25A(A).
OS *Bacillus thuringiensis* (subsp. *jegasethesan*).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=56955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawalek M.D., Gill S.S.;
RT "Isolation and characterization of insecticidal genes from *Bacillus thuringiensis* subsp. *jegasethesan*.";
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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DR EMBL: U88189; AAC61892.1; -
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 675 AA; 75642 MW; 509CC9F1F7501459 CRC64;

Query Match 1.7%; Score 11; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLDL 279
DB 277 RREMTLVLDL 287

RESULT 8

ID C9DA_BACUH STANDARD: PRT: 682 AA.
AC 086170;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry19Ba (insecticidal delta-endotoxin
DE CRY19Ba(a)) (Crystalline entomocidal protoxin) (78 kDa crystal
DE protein).
GN CRY19Ba OR CRY19Ba(A).
OS Bacillus thuringiensis (subsp. higo).
OC Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=132267;

RN SEQUENCE FROM N.A.
RX MEDLINE:98369730; PubMed:9704107;
RA Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Ohba M.;
RT "A novel class of mosquitocidal delta-endotoxin, Cry19B, encoded by a
RT Bacillus thuringiensis serovar higo gene.";
RL Syst. Appl. Microbiol. 21:179-184(1998).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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DR EMBL: D88381; AAA32397.1; -
DR HSSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation; Plasmid.
SQ SEQUENCE 682 AA; 78490 MW; 5351EA63E2B042F7 CRC64;

Query Match 1.6%; Score 10; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 FNRRTREMTL 274
DB 258 FNRRTREMTL 267

RESULT 9

ID C8BA_BACUK STANDARD: PRT: 1169 AA.
AC 045705;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry8Ba (insecticidal delta-endotoxin
DE CRY8Ba(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
DE protein).
GN CRY8Ba OR CRY8Ba(A) OR 50C(B).
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=132267;

RN SEQUENCE FROM N.A.
RC STRAIN-NRRL B-18746 / PS50C;
RA Michaels T.E., Fencera L., Narva K.E.;
RT "Process for controlling scarab pests with Bacillus thuringiensis
RT isolates.";
RL Patent number WO9315206, 05-AUG-1993.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABEID BEETLES.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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DR EMBL: U04365; AAA21118.1; -
DR HSSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1169 AA; 133543 MW; 22EEFCE5BD699909 CRC64;

Query Match 1.6%; Score 10; DB 1; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLDL 278
DB 272 RREMTLVLDL 281

RESULT 10

ID C9DA_BACTP STANDARD: PRT: 1169 AA.
AC 006014;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry9Da (insecticidal delta-endotoxin
DE CRY9Da(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
DE protein).
GN CRY9Da OR CRY9Da(A).
OS Bacillus thuringiensis (subsp. japonensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=128936;

RN SEQUENCE FROM N.A.
RP STRAIN-N141;
RC STRAIN-N141;

RA Asano S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC
 DR EMBL; D85560; BAA1948.1; -
 DR HSSP; P07130; IDLC.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1169 AA; 659AB257229DE5E9 CRC64;
 Query Match 1.6%; Score 10; DB 1; Length 1169;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 509 ITQLPYKAY 518
 Db 531 ITQLPYKAY 540
 RESULT 11
 COA_BACTU STANDARD; PRT; 674 AA.
 AC 087905;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry24Aa (insecticidal delta-endotoxin
 DE CryXIVa(a)) (Crystalline entomocidal protoxin) (Crystal protein)
 DE (insecticidal protein Jegg72) (Fragment).
 GN CRY24AA OR CRYXXIVA(A).
 OS Bacillus thuringiensis (subsp. jegathesan).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=56955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawalek M.D., Gill S.S.;
 RT "Isolation and characterization of insecticidal genes from Bacillus
 RT thuringiensis subsp. jegathesan";
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC
 DR EMBL; U88188; AAC61891.1; -

DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 FT NON-TER 674 674
 SQ SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;
 Query Match 1.4%; Score 9; DB 1; Length 674;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 635 IDKIEFIPV 643
 Db 640 IDKIEFIPV 648
 RESULT 12
 CRAA_BACUH STANDARD; PRT; 826 AA.
 AC 095597;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry27Aa (insecticidal delta-endotoxin
 DE CryXXVIIa(a)) (Crystalline entomocidal protoxin) (94 kDa crystal
 DE protein).
 GN CRY27AA OR CRYXXVIIA(A).
 OS Bacillus thuringiensis (subsp. higo).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=132266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saitoh H.;
 RT "94kDa mosquitocidal toxin from serovar higo";
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC
 DR EMBL; AB023293; BAA82796.1; -
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 826 AA; 94434 MW; DFD5313C5B6023E2 CRC64;
 Query Match 1.4%; Score 9; DB 1; Length 826;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 635 IDKIEFIPV 643
 Db 674 IDKIEFIPV 682
 RESULT 13
 C9CA_BACTO STANDARD; PRT; 1157 AA.
 ID C9CA_BACTO
 AC 045733;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry9Ca (Insecticidal delta-endotoxin
DE cry9Ca(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein).
GN CRY9CA OR CRY9CA(A).
OS *Bacillus thuringiensis* (subsp. *tolworthi*).
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-BT502618A;
RA MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Jansens S., Piens C., Saey B.,
RA Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peteren M.:
RT "A *Bacillus thuringiensis* insecticidal crystal protein with a high
RT activity against members of the family Noctuidae."
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
CC PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
CC BEETLE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL: Z37527; CAA85764.1; -
CC DR HSSP: P07130; IDLC.
CC DR InterPro: IPR001178; Endotoxin.
CC DR Pfam: PF00555; endotoxin; 1.
CC KW Toxin; Sporulation.
CC SQ SEQUENCE 1157 AA; 129775 MW; C364391EF7FDEB8A CRC64;
Query Match 1.4%; Score 9; DB 1; Length 1157;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 509 ITQPLPVKA 517
DB 515 ITQPLPVKA 523
RESULT 14
CHAA_CLOBI
ID CHAA_CLOBI STANDARD; PRT; 618 AA.
AC 005102;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal-like protein cry17Aa (insecticidal toxin
DE cry17Aa(a)) (cbm72 mosquitoicidal toxin).
GN CRY17AA OR CRYVIIA(A) OR CBM72.
OS Clostridium bifermentans.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1490;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CH18 / subsp. *Malaysia*;
RX MEDLINE=98267211; PubMed=9602158;
RA Barloy F., Decadet M.-M., Delecluse A.;

RT "Cloning and sequencing of three new putative toxin genes from
RT Clostridium bifermentans CH18.";
RL Gene 211:293-299(1998).
CC -1- FUNCTION: NOT SIGNIFICANTLY TOXIC TO MOSQUITO LARVAE MAY INCREASE
CC THE TOXICITY OF THE PESTICIDAL CRYSTAL-LIKE PROTEIN CRY16Aa
CC (CBM71).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DEVELOPMENTAL STAGE: PRODUCED DURING SPOULATION.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL: X99478; CAA67841.1; -
CC DR InterPro: IPR001178; Endotoxin.
CC DR Pfam: PF00555; endotoxin; 1.
CC KW Toxin; Sporulation.
CC FT DOMAIN 174 179 POLY-LEU.
CC SQ SEQUENCE 618 AA; 71651 MW; 1B9C5251B9AD329D CRC64;
Query Match 1.2%; Score 8; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 635 IDKIEFIP 642
DB 609 IDKIEFIP 616
RESULT 15
CTAA_BACTU
ID CTAA_BACTU STANDARD; PRT; 1138 AA.
AC 003749;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry7Aa (insecticidal delta-endotoxin
DE cry7Aa(a)) (Crystalline entomocidal protoxin) (129 kDa crystal
DE protein).
GN CRY7AA OR CRYVIIA(A) OR CRYIIIC.
OS *Bacillus thuringiensis*.
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92384571; PubMed=1514800;
RA Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peteren M.:
RT "Novel *Bacillus thuringiensis* insecticidal crystal protein with a
RT silent activity against coleopteran larvae."
RL Appl. Environ. Microbiol. 58:2536-2542(1992).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE
CC AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC -----

CC -----
 DR EMBL; M64478; AAA22351.1; -;
 DR EMBL; A07236; CAA00646.1; -;
 DR HSSP; P07130; IDLC.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SO SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;

Query Match 1.2%; Score 8; DB 1; Length 1138;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 451 DSIDQLPP 458
 |||||
 Db 438 DSIDQLPP 445

Search completed: January 10, 2003, 11:09:50
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:09 : Search time 37 Seconds
(without alignments)
3586.334 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MNPNRSEHDITKTENNENY.....TGLSAGDKYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_21:
1: sp._archaea:
2: sp._bacteria:
3: sp._fungi:
4: sp._human:
5: sp._invertebrate:
6: sp._mammal:
7: sp._mhc:
8: sp._organelle:
9: sp._phage:
10: sp._plant:
11: sp._rodent:
12: sp._virus:
13: sp._vertebrate:
14: sp._unclassified:
15: sp._virus:
16: sp._bacteriophage:
17: sp._archaeo:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	652	2	Q9S6N9
2	50	7.8	652	2	P81518
3	10	1.6	645	2	Q9S603
4	10	1.6	660	2	Q8R066
5	10	1.6	666	2	Q8VW62
6	9	1.4	239	2	Q86287
7	9	1.4	638	2	Q87654
8	9	1.4	719	2	Q9F0P8
9	9	1.4	1254	2	Q8VUL0
10	8	1.2	138	5	Q9N6M1
11	8	1.2	260	16	Q50779
12	8	1.2	294	17	Q91PD3
13	8	1.2	326	17	Q97C11
14	8	1.2	329	16	Q97D92
15	8	1.2	357	16	Q8YVR1
16	8	1.2	375	16	Q9RXS7

17	8	1.2	483	16	Q9S242	Q9S242 streptomyces
18	8	1.2	485	2	Q8VQ48	Q8VQ48 escherichia
19	8	1.2	555	2	Q9R03	Q9R03 rhizobium e
20	8	1.2	753	5	Q9VL20	Q9VL20 drosophila
21	8	1.2	760	5	Q22235	Q22235 caenorhabditis
22	8	1.2	798	5	Q9VLY9	Q9VLY9 drosophila
23	8	1.2	1144	2	Q45745	Q45745 bacillus th
24	8	1.2	1270	2	Q8VUL1	Q8VUL1 bacillus th
25	8	1.2	1420	5	Q9NFV7	Q9NFV7 drosophila
26	8	1.2	1905	3	Q92225	Q92225 emericella
27	8	1.2	3729	2	Q33956	Q33956 streptomyces
28	7	1.1	57	16	Q8X9U7	Q8X9U7 escherichia
29	7	1.1	72	5	Q61997	Q61997 brugia pah
30	7	1.1	85	2	Q51815	Q51815 bacillus su
31	7	1.1	89	16	Q92EC3	Q92EC3 listeria in
32	7	1.1	114	17	Q96Y21	Q96Y21 sulfolobus
33	7	1.1	130	11	Q9DC39	Q9DC39 mus musculu
34	7	1.1	133	4	Q9NSM7	Q9NSM7 homo sapien
35	7	1.1	137	11	Q9EON1	Q9EON1 mus musculu
36	7	1.1	140	16	Q92B66	Q92B66 listeria in
37	7	1.1	140	16	Q8V6P1	Q8V6P1 listeria in
38	7	1.1	144	4	Q96J55	Q96J55 homo sapien
39	7	1.1	153	11	Q8VEQ3	Q8VEQ3 mus musculu
40	7	1.1	162	16	Q9X812	Q9X812 streptomyces
41	7	1.1	163	16	Q91OV9	Q91OV9 streptomyces
42	7	1.1	169	4	Q9Y6E5	Q9Y6E5 homo sapien
43	7	1.1	194	16	Q8ZAE8	Q8ZAE8 yersinia pe
44	7	1.1	196	5	Q9VG7	Q9VG7 drosophila
45	7	1.1	201	11	Q9EON0	Q9EON0 mus musculu

ALIGNMENTS

RESULT 1

ID Q9S6N9 PRELIMINARY; PRT; 652 AA.
AC Q9S6N9; 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-JUN-2001 (TREMURel. 17, Last annotation update)
DE Cry3Aa protein.
GN CRY3AA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT22;
RA Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;
RT "A novel cry3Aa gene."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ237900; CAB41411.1; -.
DR HSSP; P07130; IDIC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 652 AA; 74035 MM; 544AE16E1D0F7647 CRC64;

Query Match 100.0%; Score 644; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MNPNRSEHDITKTENNENYPTNHQVYLAETPNPTLEDLNYKEFLRWTDADNTEALDSS 60
|||||
9 MNPNRSEHDITKTENNENYPTNHQVYLAETPNPTLEDLNYKEFLRWTDADNTEALDSS 68
|||||
61 TTKDVIQKISVVGDLGVGPFPGALVSTYTNPLNTINISSEDPKAFMGOVVALDOK 120
|||||
69 TTKDVIQKISVVGDLGVGPFPGALVSTYTNPLNTINISSEDPKAFMGOVVALDOK 128
|||||
121 IADYAKNKLAELQGNVVEYVALSSWKNPVSNNPHSGGRIRLEFQAQSHFRNS 180
|||||

Db 129 IADYAKKALAELOGIIONNEDVVSALSSWOKNPVSRNPHSOGIRIREFSOAESHFRRS 188
 QY 181 MPSEAISSYEVLEFLTYTAQAANTHFLFKDAOLYGEEMGEKEDIAEFKROLKLTQETT 240
 Db 189 MPSEAISSYEVLEFLTYTAQAANTHFLFKDAOLYGEEMGEKEDIAEFKROLKLTQETT 248
 QY 241 DHCKKYNVGLDKLRSSSYSWNPNRRREMTLVLDLALFPLVDVRLYPEKTELT 300
 Db 249 DHCKKYNVGLDKLRSSSYSWNPNRRREMTLVLDLALFPLVDVRLYPEKTELT 308
 QY 301 RDVLTDIVGVNLDKRGTFESNIENYIKRPHFDVLIQHTFRQPGYVNDSEFNTWS 360
 Db 309 RDVLTDIVGVNLDKRGTFESNIENYIKRPHFDVLIQHTFRQPGYVNDSEFNTWS 368
 QY 361 GNVSTRPSIGSDIITSPYKSGSEPVONLEFNGEKYRAVANTNLAVPNAVYSGVT 420
 Db 369 GNVSTRPSIGSDIITSPYKSGSEPVONLEFNGEKYRAVANTNLAVPNAVYSGVT 428
 QY 421 KVEFSYNDQTDASOTYDSDKRVNGAVSWDSIDOLPEPTTDEPLEKGYSHQANVMCFL 480
 Db 429 KVEFSYNDQTDASOTYDSDKRVNGAVSWDSIDOLPEPTTDEPLEKGYSHQANVMCFL 488
 QY 481 MOGSRGTIPVLWTNKSVDFFNMIDSKITQPLVKAYKLGASVAVGPRFTGGDIQC 540
 Db 489 MOGSRGTIPVLWTNKSVDFFNMIDSKITQPLVKAYKLGASVAVGPRFTGGDIQC 548
 QY 541 TENGAATITVTPDVSYSKYRARIHYASTQITFTSLDGAFFNOYFEDKTKNGDILT 600
 Db 549 TENGAATITVTPDVSYSKYRARIHYASTQITFTSLDGAFFNOYFEDKTKNGDILT 608
 QY 601 YNSFNLSFSPPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644
 Db 609 YNSFNLSFSPPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 652

RESULT 2

PRELIMINARY; PRT; 50 AA.
 ID P81518
 AC P81518;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE 70 kDa CRYSTAL protein (Delta endotoxin) (CRYSTALINE ENTOMOCIDAL DE PROTOXIN) (Fragment).
 GN CRYTIIA.
 OS Bacillus thuringiensis.
 OC Bacteria: Firmicutes: Bacillus/Clostridium group: Bacillales;
 CC Bacillaceae: Bacillus.
 NX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE OF 1-50 FROM N.A.
 RC STRAIN-LM79;
 RA MEDLINE-9325939; PubMed-8491716;
 RA de Souza M., Lecadet M.M., Lerecuis D.;
 RT "Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a distant upstream DNA sequence affecting transcription.";
 RL J. Bacteriol. 175:2952-2960(1993).
 CC -1- FUNCTION: PROMOTES COLLOIDSMORPHIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
 DR EMBL: L03393; AAA22350.1; -;
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 KW Toxin; Sporulation.
 FT NON_TER 50
 SQ SEQUENCE 50 AA; 5829 MW; 9AA1FD4DFC7B808 CRC64;

Query Match

Best Local Similarity 7.8%; Score 50; DB 2; Length 50;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNNEVPTNHVQYPLAEFPNPTLEDLANKKEFLRMWA 50

Db 1 MNPNNRSEHDTIKTTENNNEVPTNHVQYPLAEFPNPTLEDLANKKEFLRMWA 50

RESULT 3

PRELIMINARY; PRT; 645 AA.
 ID 09S603
 AC 09S603;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Delta-endotoxin (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria: Firmicutes: Bacillus/Clostridium group: Bacillales;
 CC Bacillaceae: Bacillus.
 NX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROVAR JAPONENSIS TYPE.
 RX MEDLINE-99025985; PubMed-9806979;
 RA Masano N., Ohda M.;
 RT Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal inclusions.";
 RT Curr. Microbiol. 37:408-411(1998).
 DR EMBL: AF042733; AAB97923.1; -;
 DR HSP: P07130; IDIC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 FT NON_TER 1
 SQ SEQUENCE 645 AA; 72967 MW; 143E51312B890C83 CRC64;

Query Match 1.6%; Score 10; DB 2; Length 645;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 ITQPLPVKAY 518
 Db 516 ITQPLPVKAY 525

RESULT 4

PRELIMINARY; PRT; 660 AA.
 ID 08R006
 AC 08R006;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Insecticidal crystal protein bun2 (Fragment).
 GN CRYBUN2.
 OS Bacillus thuringiensis.
 OC Bacteria: Firmicutes: Bacillus/Clostridium group: Bacillales;
 CC Bacillaceae: Bacillus.
 NX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ito T., Sahara K., Asano S., Bando H.;
 RT "Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawa Encoding a Mosquitocidal Proteins.";
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB074413; BAB72016.2; -;
 FT NON_TER 1
 SQ SEQUENCE 660 AA; 75643 MW; A92EF6257C2B9404 CRC64;

Query Match 1.6%; Score 10; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 VYIDKIEFIP 642
 Db 624 VYIDKIEFIP 633

RESULT 5
 Q8VM62 PRELIMINARY: PRT: 666 AA.
 AC Q8VM62:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Insecticidal crystal protein bun3 (Fragment).
 GN CRYBUN3.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ito T., Sahara K., Asano S., Bando H.;
 RT "Cloning and Expression of Novel Crystal Protein Genes from Bacillus
 thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB074414; BAB72018.1; -;
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 666 AA; 75311 MW; A87853FAE8FAA1D CRC64;
 Query Match 1.6%; Score 10; DB 2; Length 666;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 269 RREMTLVLD 278
 DB 280 RREMTLVLD 289

RESULT 6
 Q86287 PRELIMINARY: PRT: 239 AA.
 AC Q86287:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 27.6 kDa protein.
 GN ORC.
 OS Lactococcus lactis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-N8; TRANSPOSON-TN5481;
 RC MEDLINE-94452384; PubMed-10524753;
 RA Immonen T., Wahlstrom G., Takala T., Saris P.E.J.;
 RT "Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis
 N8.";
 RT DNA Seq. 9:245-261(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-N8; TRANSPOSON-TN5481;
 RC MEDLINE-94452385; PubMed-10524754;
 RA Immonen T., Saris P.E.J.;
 RT "Characterization of the nlsFEG operon of the nlsin 2 producing
 Lactococcus lactis subsp. lactis N8 strain.";
 RT DNA Seq. 9:263-274(1998).
 DR EMBL: AJ000993; CA04444.1; -;
 DR InterPro: IPR000160; GSDEF.
 DR Pfam: PF00990; GSDEF; 1.
 DR SMART: SM00267; DUF1.1.
 DR TIGRFAWS: TIGR00254; GSDEF; 1.
 KW Hypothetical protein; Plasmid.

SQ SEQUENCE 239 AA; 27630 MW; 96E3258044D23FD CRC64;
 Query Match 1.4%; Score 9; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 320 TFSNIENYI 328
 DB 209 TFSNIENYI 217

RESULT 7
 Q87654 PRELIMINARY: PRT: 638 AA.
 AC Q87654:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Delta-endotoxin (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-92-KU-149-8;
 RC MEDLINE-21064760; PubMed-11136135;
 RA Wasano N., Ohba M., Miyamoto K.;
 RT "Two delta-Endotoxin Genes, cry9Da and a Novel Related Gene, Commonly
 occurring in Lepidoptera-Specific Bacillus thuringiensis Japanese
 RT Isolates that Produce Spherical Parasporal Inclusions.";
 RL Curr. Microbiol. 42:129-133(2001).
 DR EMBL: AF093107; AAC63366.1; -;
 DR HSSP: P07130; IDLC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 FT NON_TER 1
 SQ SEQUENCE 638 AA; 71993 MW; 1817831FEF080A61 CRC64;
 Query Match 1.4%; Score 9; DB 2; Length 638;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 509 ITQLPLVKA 517
 DB 509 ITQLPLVKA 517

RESULT 8
 Q9F0P8 PRELIMINARY: PRT: 719 AA.
 AC Q9F0P8:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Cry11.
 GN CRY11.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BTC007;
 RC Song F., Zhang J., Huang D., Li G.;
 RT "The cloning of a novel cry11 gene from Bacillus thuringiensis
 strain.";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF211190; AA643526.1; -;
 DR HSSP: P02965; IC1Y.
 DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

KW Plasmid.

SO SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 1.4%; Score 9; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 276 VLDIALFP 284

DB 268 VLDIALFP 276

RESULT 9

08VUL0 PRELIMINARY; PRT; 1254 AA.

AC 08VUL0;

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

GN CRYE60.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA Takebe S., Matsumura T., Izumoto Y., Komano T.;

RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB075461; BAB78602.1; -

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

SO SEQUENCE 1254 AA; 143534 MW; BD35AB7653CF12DC CRC64;

Query Match 1.4%; Score 9; DB 2; Length 1254;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 635 IDKIEPIV 643

DB 657 IDKIEPIV 665

RESULT 10

09N6M1 PRELIMINARY; PRT; 138 AA.

AC 09N6M1;

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE Mod(mdg4)54.6 (Fragment).

GN MOD(mdg4) OR CG7836 OR CG8076 OR CG15802.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20253099; PubMed=10790390;

RA Buechner K., Roth P., Schotta G., Krauss V., Saumweber H., Reuter G.,

RA Dorn R.;

RT "Genetic and molecular complexity of the position effect variegation

RT Genetics 155:141-157(2000)."

RL EMBL; AJ277178; CAB85473.1; -

DR FlyBase; FBgn0002781; mod(mdg4).

FT NON_TER

SO SEQUENCE 138 AA; 15414 MW; F8326FED6FC2C42 CRC64;

Query Match 1.2%; Score 8; DB 5; Length 138;

Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 302 DVLTDPV 309

DB 46 DVLTDPV 53

RESULT 11

050779 PRELIMINARY; PRT; 260 AA.

AC 050779;

DT 01-JUN-1998 (TREMblrel. 06, Created)

DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)

DE Hypothetical protein BBJ24.

GN BBJ24.

OS Borrelia burgdorferi (Lyme disease spirochete).

OG Plasmid lp38.

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI_TaxID=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31;

RX MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Castens S., Huang W.M., Sutton G.G., Clayton R.A.,

RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

RA Peterson J., Kervatage A.R., Quackenbush J., Salzberg S., Hanson M.,

RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

RA Ullrich S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

RA Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochete, Borrelia

RT burgdorferi."

RL Nature 390:580-586(1997).

DR EMBL; AE000787; AAC66120.1; -

DR TIGR; BBJ24; -

KW Hypothetical protein; Plasmid; Complete proteome.

SO SEQUENCE 260 AA; 30484 MW; B0102AF885DCBE CRC64;

Query Match 1.2%; Score 8; DB 16; Length 260;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 632 KYIDKIE 639

DB 22 KYIDKIE 29

RESULT 12

091FD3 PRELIMINARY; PRT; 294 AA.

AC 091FD3;

DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

GN 391R.

OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).

OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.

OX NCBI_TaxID=10488;

RN [1]

RP SEQUENCE FROM N.A.

RA Drell H., Darai G., Fluegel R.M.;

RT "DNA analysis of insect iridescent virus 6: evidence for circular

RT permutation and terminal redundancy."

RL J. Virol. 49:609-614(1984).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86174607; PubMed=3959991;

RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;

RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis

RT in mice."

RL Med. Microbiol. Immunol. 175:43-53(1986).
 RP SEQUENCE FROM N.A.
 RA MEDLINE-87321126; PubMed-2820141;
 RA Schiltzler P., Soltan J.B., Fischer M., Relander H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 RT iridescent virus type 6: further evidence for circular permutation of
 RT the viral genome.";
 RL Virology 160:66-74(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89073752; PubMed-3201750;
 RA Fischer M., Schiltzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 RT the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92196996; PubMed-1549908;
 RA Handermann M., Schiltzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93118242; PubMed-1475907;
 RA Sonntag K.C., Darai G.;
 RT "Characterization of the third origin of DNA replication of the genome
 RT of insect iridescent virus type 6.";
 RL Virus Genes 6:333-342(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93260401; PubMed-8492091;
 RA Stohwasser R., Raab K., Schiltzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94167241; PubMed-8121799;
 RA Schiltzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN [9]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94353641; PubMed-8073636;
 RA Sonntag K.C., Schiltzler P., Koonin E.V., Darai G.;
 RT "Chilo iridescent virus encodes a putative helicase belonging to a
 RT distinct family within the 'Dead/H' superfamily: implications for the
 RT evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
 RN [10]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-95213160; PubMed-7698884;
 RA Sonntag K.C., Schiltzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of
 RT the genome of insect iridescent virus type 6 between the genome
 RT coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 RN [11]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94292906; PubMed-8021587;
 RA Schiltzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
 RA Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the
 RT largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN [12]

RP SEQUENCE FROM N.A.
 RA MEDLINE-98141693; PubMed-9482589;
 RA Bahr U., Tildona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 RT coordinates 0.101 and 0.391: similarities in coding strategy between
 RT insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99125223; PubMed-9926400;
 RA Muller K., Tildona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of
 RT Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN [14]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99383793; PubMed-10456793;
 RA Muller K., Tildona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264(1999).
 RN [15]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21342589; PubMed-11448171;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the First Complete DNA Sequence of an Invertebrate
 RT Iridovirus: Coding Strategy of the Genome of Chilo Irdescent Virus.";
 RL Virology 286:182-196(2001).
 RN [16]
 RP SEQUENCE FROM N.A.
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF303741; AAK82251.1; -
 DR InterPro: IPR000822; Znf C2H2.
 DR Pfam: PF00096; Zf-C2H2; 1.
 KW DNA-binding; Zinc-finger.
 SQ SEQUENCE 294 AA; 34614 MW; 761C8CE489CE86D CRC64;
 Query Match 1.2%; Score 8; DB 12; Length 294;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 462 DEPLEXGY 469
 Db 68 DEPLEXGY 75
 RESULT 13
 Q97C11
 ID Q97C11 PRELIMINARY; PRT; 326 AA.
 AC Q97C11;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Hypothetical protein TV0294.
 GN TV0294 OR TVG0304564.
 OS Thermoplasma volcanium.
 OC Archaea: Euryarchaeota: Thermoplasmata: Thermoplasmatales;
 OC Thermoplasmataceae: Thermoplasma.
 OX NCBI_Taxid=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GSSI / DSM 4299 / JCM 9571;
 RC MEDLINE-20570466; PubMed-11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Aramaki H., Makino K., Kaneshiro K.,
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 RT sequence of Thermoplasma volcanium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL: AP000992; BAB59436.1; -
 DR InterPro: IPR001387; HTR_3.

DR Pfam; PF01381; HTH_3; 1.
 DR SMART; SM00530; HTH_XRE; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 326 AA; 36773 MW; D10685EEEC08C931 CRC64;

Query Match 1.2%; Score 8; DB 17; Length 326;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 ENGSAATI 549
 DB 176 ENGSAATI 183

RESULT 14
 O97D92 PRELIMINARY; PRT; 329 AA.

AC O97D92.
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE DNA replication protein DnaC.
 GN CAC3588.
 OS Clostridium acetobutylicum.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 CC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
 RA Tatusev R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007855; AAK81511.1; -.
 KW Complete proteome.
 SQ SEQUENCE 329 AA; 36693 MW; 91578425D5C2958E CRC64;

Query Match 1.2%; Score 8; DB 16; Length 329;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 PNPTLEDL 40
 DB 235 PNPTLEDL 242

RESULT 15
 O8YVRI

AC O8YVRI PRELIMINARY; PRT; 357 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 6-phosphofructokinase.
 GN ALR1913.
 OS Anabaena sp. (strain PCC 7120).
 CC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21595285; PubMed-11759840;
 RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iritani M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120";

RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003587; BAB73612.1; -.
 DR InterPro; IPR000023; PpfFructKinase.
 DR Pfam; PF00365; Pfk_1
 DR PRINTS; PR00476; PFERCTKINASE.
 DR ProDom; PD000707; PpfFructKinase; 1.
 DR PROSITE; PS00433; PHOSPHOFRICTOKINASE; 1.
 KW Kinase; Complete proteome.
 SQ SEQUENCE 357 AA; 38006 MW; 40A6C3C266A6E5D0 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 357;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 592 TINKGDTL 599
 DB 77 TINKGDTL 84

Search completed: January 10, 2003, 11:10:35
 Job time : 39 secs